

178157

STIC-Biotech/ChemLib

From: Whiteman, Brian  
Sent: Tuesday, January 31, 2006 1:19 PM  
To: STIC-Biotech/ChemLib  
Subject: seq search

10/800,256

SEQ ID NO: 1  
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Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

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\*\*\*\*\*  
Searcher: \_\_\_\_\_  
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Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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FT CDS (3290) . (4384)  
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FT CDS (4544) . (6205)  
FT intron (6206) . (6411)  
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ORIGIN

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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ACCESSION AR492934  
VERSION AR492934.1 GI:47264085  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15186)  
AUTHORS Peeters,B.P.H., de Leeuw,O.S. and Gielkens,A.L.J.  
TITLES Newcastle disease virus infectious clones, vaccines and diagnostic assays  
JOURNAL Patent: US 6719979-A 134 13-APR-2004;  
ID=Leijstcad, Instituut voor Dieronderij en Diergezondheid B.V.;  
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FEATURES  
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FEATURES	Source
TITLE	Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL	Patent : WO 996045-A 162 23-DEC-1999; GIELKENS ARNOLD LEONARD JOSEF (NL) ; KOCH GUS (NL) ; LEEUW OLAV SVEN DE (NL) ; PEETERS BERNARDUS PETRUS HUBER (NL) ; STICHTING DIENST LANDBOUWINDUSTRIE (NL)
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CDS

Intron  
CDS

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VERSION AF077761.1 GI:3386504  
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ORGANISM Newcastle disease virus  
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Paramyxoviridae; Paramyxovirinae; Avulavirinae.  
REFERENCE  
1 (bases 1 to 15186)  
de Leeuw, O. and Peeters, B.  
Complete nucleotide sequence of Newcastle disease virus: evidence  
for the existence of a new genus within the subfamily  
Paramyxovirinae  
J. Gen. Virol. 80 (Pt 1), 131-136 (1999)  
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2 (bases 1 to 15186)  
de Leeuw, O.S. and Peeters, B.P.H.  
Direct Submission  
Submitted (14-JUL-1998) Avian Virology, Institute for Animal  
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SOURCE Newcastle disease virus  
ORGANISM Newcastle disease virus  
viriuses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.  
REFERENCE 1 Romer-Oberdorfer, A., Mundt, E., Mebatsion, T., Buchholz, U.J. and Mettenleiter, T.C.  
Generation of recombinant lentogenic Newcastle disease virus from cDNA  
JOURNAL U. Gen. Virol. 80 (Pt 11), 2987-2995 (1999)  
PUBMED 10580061  
REFERENCE 2 (bases 1 to 15186)



AUTHORS Romer-Oberdorfer, A.  
TITLE Direct Submission  
JOURNAL Submitted (31-MAR-1999) A. Romer-Oberdorfer, Federal Research  
Centre for, Virus Diseases of Animals, Insel Riem, D-17498, FRG

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LOCUS Newcastle disease virus strain HB92 isolate V4, complete genome.  
DEFINITION AY225110  
ACCESSION AY225110  
VERSION AY225110.1 GI:28824865  
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SOURCE Newcastle disease virus  
ORGANISM Newcastle disease virus  
Virus; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirinae.  
REFERENCE  
1 (bases 1 to 15186)  
Pan, Z. S., Chen, Y. D., Shao, H. B., Yang, J., Xiong, Z. L., Wen, G. Y. and  
Zhang, C. Y.  
Complete sequence for HB92 strain of Newcastle disease virus  
JOURNAL Unpublished  
REFERENCE  
2 (bases 1 to 15186)  
Pan, Z. S., Chen, Y. D., Wen, G. Y. and Zhang, C. Y.  
Direct Submission  
JOURNAL Submitted (23-JUN-2003) Institute of Virology, Department of Life  
Science, Wuhan University, Wuhan, Hubei 430072, China  
REFERENCE  
3 (bases 1 to 15186)  
Shao, H. B., Yang, J. and Xiong, Z. L.  
Direct Submission  
JOURNAL Submitted (23-JUN-2003) Institute of Animal Husbandry and  
Veterinary Science, Hubei Academy of Agricultural Science, Wuhan,  
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FEATURES  
Location/Qualifiers

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Bu, Z., Ge, J., Hu, S. and Wen, Z.  
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ACCESSION AP375823  
VERSION AP375823.1 GI:14190062  
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SOURCE Newcasttle disease virus B1  
ORGANISM Viruses; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulaviruses.  
REFERENCE Nakaya,T., Cros,J., Park,M.S., Nakaya,Y., Zheng,H., Sagretera,A.,  
AUTHORS Villar,E., Garcia-Sastre,A. and Palese,P.  
TITLE Recombinant Newcasttle disease virus as a vaccine vector  
JOURNAL J. Virol. 75 (23), 11868-11873 (2001)  
PUBMED 11689668  
RECORD 2 (bases 1 to 15186)  
AUTHORS Nakaya,T., Garcia-Sastre,A. and Palese,P.  
TITLE Direct Submission  
JOURNAL Submitted (02-MAY-2001) Microbiology, Mount Sinai School of  
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## ORIGIN

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Matches 3327;	Conservative	0;	Mismatches 31;	Indels 0;
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Qy 3181 CCCCGTTATTTATATCTTATGACAGTCAAGCAACAAAACGCACTTTCATATGCTTAT 3240  
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Db	Accession	Length	Source
3301	AACTCGTGTCTACGAGGATCTATACATTCATATCCCGTAATCTTATAGAAACC	3358	NC_009418.1
7798	AACTCGTGTCTACGAGGATCTATACATTCATATCCCGTAATCTTATAGAAACC	7855	NC_009418.1
RESULT 9			
LOCUS	AF309418	15186 bp	RNA linear VRL 02-DEC-2000
DEFINITION	Newcastle disease virus B1, complete genome.		
ACCESSION	AF309418		
VERSION	AF309418.1		
KEYWORDS			
SOURCE			
ORGANISM	Newcastle disease virus B1 Virus; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulaviruts.		
REFERENCE	1 (bases 1 to 15186) Sellers,H.S. and Seal,B.S. Complete sequence for the B1 strain of Newcastle disease virus		
AUTHORS	2 (bases 1 to 15186) Sellers,H.S. and Seal,B.S.		
TITLE	Direct Submission		
REFERENCE	Submitted (28-SEP-2000) U.S. Department of Agriculture/Agriculture Research Services, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
JOURNAL	Location/Qualifiers		
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ORIGIN

Query Match 98.4%; Score 3305.2; DB 13; Length 15186;  
Best Local Similarity 99.0%; Pred. No. 0; Mismatches 33; Indels 0; Gaps 0;  
Matches 3325; Conservative 0;

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Qy	181	AGGAGACAAAGCCGTCAACATATACACTCATCCAGACAGATCATATGTTAAAGCT	240
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Qy	301	CAGACATTTGACCACTTTGCTCAACCCCTTGGTGACTCTATCCGTAGGATRCAAGAGTC	360
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Qy	1741	TAAATTTGGGAAGTTCTGTTAGTCTGTCAAGTTCAGAGATTAAGAAAAAATCAACGGT	1800
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Db 7618 AGAATTTCAAGATGAGGACATCTTCTTGTATCAAGAGGTCATCAATCTTCT 7677  
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RESULT 10  
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DEFINITION  
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ACCESSION  
AY289002  
VERSION  
AY289002.1  
KEYWORDS  
GI:33772483  
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Newcastle disease virus  
ORGANISM  
Newcastle disease virus  
REFERENCE  
1 (bases 1 to 3819)  
Seal, B.S.  
Nucleotide and predicted amino acid sequence analysis of the fusion protein and hemagglutinin-neuraminidase protein genes among Newcastle disease virus isolates. Phylogenetic relationships among the Paramyxovirinae based on attachment glycoprotein sequences  
Func. Integr. Genomics 4 (4), 246-257 (2004)  
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JOURNAL  
PUBMED  
2 (bases 1 to 3819)  
Seal, B.S.  
Direct Submission  
REFERENCE  
Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA  
JOURNAL  
TITLE  
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Location/Qualifiers  
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## RESULT 11

A03663 3825 bp DNA linear PAT 14-Apr-2005  
LOCUS  
DEFINITION Newcastle disease virus HN and F genes.  
ACCESSION A03663  
VERSION A03663.1 GI:492839  
KEYWORDS  
SOURCE  
ORGANISM Newcastle disease virus  
Viruses; ssRNA negative-strand viruses; Mononegavirales;  
Paramyxoviridae; Paramyxovirinae; Avulavirinae.

## REFERENCE

1 (bases 1 to 3825)  
Bingham, R.W., Chambers, P., Emerson, P.T. and Millar, N.S.  
Newcastle disease virus gene clones  
Patent: EP 0227414-A 2 01-JUL-1987;  
NATIONAL RESEARCH DEVELOPMENT CORPORATION  
location/Qualifiers

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## ORIGIN

Query Match 95.3%; Score 3199.6; DB 6; Length 3825;  
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DEFINITION Newcastle disease virus, complete genome.  
ACCESSION DQ060053  
VERSION DQ060053.1 GI:67552898  
KEYWORDS Newcastle disease virus  
SOURCE Newcastle disease virus  
ORGANISM Newcastle disease virus  
Virus; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulaviruses.  
REFERENCE 1 (bases 1 to 15186)  
Wang,Z., Bao,J., Chen,J., Zhen,D., Chen,Y. and Song,C.  
Genomic sequence for isolate AQI-ND026 of Newcastle disease virus  
Unpublished  
2 (bases 1 to 15186)  
Wang,Z., Bao,J., Chen,J., Zhen,D., Chen,Y. and Song,C.  
Direct Submission  
Submitted (10-MAY-2005) National Exotic Animal Disease Center,  
National Animal Quarantine Institute, Ministry of Agriculture, 369  
Nanjing Road, Qingdao, Shandong 266032, China  
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ORIGIN

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QY	2641	ACTCCCTCGGGTGTGATATGTCTGTCTGCCAAAGTCACGGACAGAGGAAGAGATAT	2700
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Db	7378	AATTCACCCAGTGAACCTGTACAGGAAGGAAATATGTATATATACGAGTACATATAC	7437
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QY	3241	ACATTCAATGCTTCACTTCGGCCAGGTATATCCCTTCCAGGGCTTCAGCAAGATGCCCC	3300
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QY	3301	AACCTGCTGTATCTGAGGTCTATACATCCATATCCCTTATCTTATATGAATCC	3358
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RESULT 13					
LOCUS	E01252	3825 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	Synthetic DNA encoding Newcastle disease virus (NDV) protein.				
ACCESSION	E01252				
VERSION	E01252.1	GI:2169511			
KEYWORDS	JP 1987163693-A/1.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 3825)				
AUTHORS	Richiyoado,U.B., FuiritsuPU,C., Pitaa,T.E. and Neiru,S.M.				
TITLE	NEWCASTLE DISEASE VIRUS GENE CLONE				
JOURNAL	Patent: JP 1987163693-A 1 20-JUL-1987; NATL RES DEV CORP				
COMMENT	OS Artificial gene OC Artificial sequence; Genes. OS Newcastle disease virus (NDV) PN JP 1987163693-A/1 PD 20-JUL-1987 PF 18-DEC-1986 JP 1986302719 PR 18-DEC-1985 GB 85 8531147, 14-APR-1986 GB 86 8609037, PR 15-JUL-1986 US 86 865765 PI RICHIIYADO UOOKAA BINGAMU, FUIRITSUPU CHIYANBAZU, PI PITAA TANREI EMASON, PI NEIRU SUTEXUMATO MIRAA PC C12N15/00 C12N1/20//A61K39/17, C12P21/02, (C12N1/20, C12R1:19) ; /product='Newcastle disease virus (NDV) FT protein'				
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ORIGIN					
Query_Match	95.2%;	Score 3196.4;	DB 6;	Length 3825;	
Best Local Similarity	97.0%;	Pred. No. 0;			
Matches 3257;	Conservative	0;	Mismatches 101;	Indels	0;
				Gaps	0;
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DB	61	TTCTACCAAGAACCCAGACCTATGATGCTAATTCGGGTTGCCCTGGACCTGAGATTG	120		
QY	121	CATCGTCCGGCAAACTCATTGATGGGAGGCTCTTGACGCTCAGGAATTGGTGTAC	180		
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DB	181	AGGAGACAAAGCCGTCAACATATACCTCTACCCAGACAGATCAATCATAGTTAAGCT	240		
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RESULT 14
AY289000 4552 bp mRNA linear VRL 04-OCT-2004
LOCUS Newcasttle disease virus chicken/USA/Roakin/48 fusion protein and
DEFINITION hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
ACCESSION AY289000
VERSION AY289000.1 GI:33772477
KEYWORDS Newcasttle disease virus
SOURCE Newcasttle disease virus
ORGANISM Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Avulaviruses.

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REFERENCE 1 (bases 1 to 4552)
AUTHORS Seal,B.S.
TITLE Nucleotide and predicted amino acid sequence analysis of the fusion
protein and hemagglutinin-neuraminidase protein genes among
Newcasttle disease virus isolates. Phylogenetic relationships among
the Paramyxovirinae based on attachment glycoprotein sequences
JOURNAL Funct. Integr. Genomics 4 (4), 246-257 (2004)
PUBMED 15108051
REFERENCE 2 (bases 1 to 4552)
AUTHORS Seal,B.S.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2003) Agricultural Research Service, USDA,
Southeast Poultry Research Laboratory, 934 College Station Road,
Athens, GA 30605, USA
FEATURES
source location/Qualifiers
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## ORIGIN

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Query Match 95.0%; Score 3190; DB 13; Length 4552;
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Matches 3253; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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RESULT 15					
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LOCUS	Newcastle disease virus gene for fusion glycoprotein precursor,				
DEFINITION	haemagglutinin-neuraminidase glycoprotein precursor.				
ACCESSION	D002433				
VERSION	D002433.1 GI:222174				
KEYWORDS	haemagglutinin-neuraminidase glycoprotein precursor; fusion glycoprotein precursor; F; HN; NDV; avirulent.				
SOURCE	Newcastle disease virus				

ORGANISM Newcastle disease virus  
 Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 Paramyxoviridae; Paramyxovirinae; Avulavirinae.  
 REFERENCE 1 (bases 1 to 3825)  
 AUTHORS Millar,N.S., Chambers,P. and Emmerson,P.T.  
 TITLE Nucleotide sequence of the fusion and haemagglutinin-neuraminidase  
 glycoprotein genes of Newcastle disease virus, strain Uster:  
 molecular basis for variations in pathogenicity between strains  
 JOURNAL J. Gen. Virol. 69 (Pt 3), 613-620 (1988)  
 PUBMED 3351479

COMMENT To understand the molecular basis for the differences in virulence  
 shown by strains of NDV, the sequences of the E and HN genes of the  
 extremely virulent strain Uster were determined and compared with  
 those of several other NDV strains (discussed in [1]).

FEATURES  
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ORIGIN polyA\_signal  
 84.2%; Score 2826.8; DB 13; Length 3825;  
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 Db 2641 ACTCCCTGGGTGTGATATGCTGTCTGAAAGTCAAGAGACAGAGAAAGAAATTTAT 2700  
 QY 2701 AACTCAGCTGTCTTACGCGGATGATATGAGAGGTTAAGGTTGACAGGCGCATACAC 2760  
 Db 2701 AACTCAGCTGTCTTACGCGGATGATATGAGAGGTTAAGGTTGACAGGCGCATACCAT 2760  
 QY 2761 GAAAGGACCTAGATGTCACAACTTATTCGGGGGCTGGTGGCCCACTAACCCAGAGTA 2820  
 Db 2761 GAAAGGACCTAGATGTCACAACTTATTCGGGGGCTGGTGGCCCACTAACCCAGAGTA 2820  
 QY 2821 GGGGGGTGATCTTTTATTTGACAGCGCGTATGTTCTCAGTCTACGAGGGTTAAACC 2880  
 Db 2821 GGGGGGTGATCTTTTATTTGACAGCGCGTATGTTCTCAGTCTACGAGGGTTAAACC 2880  
 QY 2881 AATTCAACCAAGTACCTGTACAGAGAGGAAATATGATATATACAGGATACATGAC 2940  
 Db 2881 AATTCAACCAAGTACCTGTACAGAGAGGAAATATGATATATACAGGATACATGAC 2940  
 QY 2941 ACATGCCAGATGACAAAGATCAAGATTCGAATGCGCAAGTCTTGATTAAGGCTGGA 3000  
 Db 2941 ACATGCCAGATGACAAAGATCAAGATTCGAATGCGCAAGTCTTGATTAAGGCTGGA 3000  
 QY 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060  
 Db 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTTG 3060  
 QY 3061 GGGGAGAGCCGGTACTGATCTGTACCGGCCAAACACAGTCACTCATGGGGCTGAAGGC 3120  
 Db 3061 GGGGAGAGCCGGTACTGATCTGTACCGGCCAAACACAGTCACTCATGGGGCTGAAGGC 3120  
 QY 3121 AGAATTTCAAGATAGGACATCTCATTTCTTGTATCAACGAGGTCATCACTTCTCT 3180  
 Db 3121 AGAATTTCAAGATAGGACATCTCATTTCTTGTATCAACGAGGTCATCACTTCTCT 3180  
 QY 3181 CCCGCTTATATATCTATGACAGTCAAGCAAAACAGGCACTCTCATAGTCTTAT 3240  
 Db 3181 CCCGCTTATATATCTATGACAGTCAAGCAAAACAGGCACTCTCATAGTCTTAT 3240  
 QY 3241 ACATTTCAATGCTTCACTGCGCAGATGATTCCTTGCAGGCTTCAGCAAGATGCCCC 3300  
 Db 3241 ACATTTCAATGCTTCACTGCGCAGATGATTCCTTGCAGGCTTCAGCAAGATGCCCT 3300  
 QY 3301 AACTCGTGTATCTGAGTCTATACAGATCAATCCCTAATCTTCTATAGAAACC 3358  
 Db 3301 AACTCGTGTATCTGAGTCTATACAGATCAATCCCTAATCTTCTATAGAAACC 3358

Search completed: February 5, 2006, 02:40:31  
 Job time : 16571 secs

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CC The invention relates to a clonal lentogenic oncolytic strain of  
CC Newcastle Disease Virus (NDV) comprising a DNA sequence encoding for the  
CC fusion glycoprotein (F) gene and a part of the haemagglutinin-  
CC neuraminidase (HN) gene. The lentogenic oncolytic strain of NDV or a  
CC viral glycoprotein having oncolytic activity, is useful in preparing a  
CC composition for the treatment of cancer. The present sequence represents  
CC a NDV strain HUV nucleotide sequence containing all of the F gene, an  
CC intergene and most of the HN gene  
XX

Sequence 3358 BP; 984 A; 785 C; 746 G; 843 T; 0 U; 0 Other;

Query Match 100.0%; Score 3358; DB 8; Length 3358;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACGGGTGAAGATTCGTGATCCGGTTGGCGCCCTCCAGTGCAGATGGGCTCCAGACC 60
DB 1 ACGGGTGAAGATTCGTGATCCGGTTGGCGCCCTCCAGTGCAGATGGGCTCCAGACC 60
QY 61 TTCTACCAAGAACCCAGCAGCTATGATGCTGATATCCGGTTGGCGCTGGCACTGAGTTG 120
DB 61 TTCTACCAAGAACCCAGCAGCTATGATGCTGATATCCGGTTGGCGCTGGCACTGAGTTG 120
QY 121 CATCTGTCGGCAAACTTCATTTGATGGCAGGCTCTTGCAGCTGCAGGAATTGGTTAC 180
DB 121 CATCTGTCGGCAAACTTCATTTGATGGCAGGCTCTTGCAGCTGCAGGAATTGGTTAC 180
QY 181 AGGAGCAAAAGCCGTCACATATACCTCATCCAGACAGATCAATCATAGTTAAAGCT 240
DB 181 AGGAGCAAAAGCCGTCACATATACCTCATCCAGACAGATCAATCATAGTTAAAGCT 240
QY 241 CCTCCGAAATCTGCCCAAGATTAAGAGGCAATGTCGCAAAAGCCCTTGGATGCAATCA 300
DB 241 CCTCCGAAATCTGCCCAAGATTAAGAGGCAATGTCGCAAAAGCCCTTGGATGCAATCA 300
QY 301 CAGGACATTTGACCACTTTGCTCAACCCCTTGGTACTTATCCGTAGATTAACAAGATC 360
DB 301 CAGGACATTTGACCACTTTGCTCAACCCCTTGGTACTTATCCGTAGATTAACAAGATC 360
QY 361 TGTGACATCACTGAGAGGGGGGAGACAGGGGGGCTTATAGGGCCCATTTATGGCGGTG 420
DB 361 TGTGACATCACTGAGAGGGGGGAGACAGGGGGGCTTATAGGGCCCATTTATGGCGGTG 420
QY 421 GGCTCTTGGGGTTGCAACTGCGCACAATAACAGCGGCGCAGCTCTGATACAAGCCAA 480
DB 421 GGCTCTTGGGGTTGCAACTGCGCACAATAACAGCGGCGCAGCTCTGATACAAGCCAA 480
QY 481 ACAAATATGCTGCCAATCTCTCGAATTAAAGAGCAATTGCCGAACCAATGAGGCTGT 540
DB 481 ACAAATATGCTGCCAATCTCTCGAATTAAAGAGCAATTGCCGAACCAATGAGGCTGT 540
QY 541 GCATGAGGTCACTGACGATTAATGCAACTGACAGTGGCAATTTGGGAAAGATGACAGTT 600
DB 541 GCATGAGGTCACTGACGATTAATGCAACTGACAGTGGCAATTTGGGAAAGATGACAGTT 600
QY 601 TGTATATGACCAATTTATATAAAGAGCTCAGAGATTAGACTGATCAAAATTTGCACAGA 660
DB 601 TGTATATGACCAATTTATATAAAGAGCTCAGAGATTAGACTGATCAAAATTTGCACAGA 660
QY 661 AGTTGTGTAGAGCTCAACCTGTACTTACCGAATTGACTACATATTCGGAACCAAAAT 720
DB 661 AGTTGTGTAGAGCTCAACCTGTACTTACCGAATTGACTACATATTCGGAACCAAAAT 720
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTGATGTGTGAAA 780
DB 721 CACTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAACTGATGTGTGAAA 780
QY 781 TATGATTAATCTATTTAGATAGGTAGGTAGGGAACAATCAATCAGCTCATTAATCGG 840
DB 781 TATGATTAATCTATTTAGATAGGTAGGTAGGGAACAATCAATCAGCTCATTAATCGG 840
QY 841 TAGCGGCTTATCAACCGGTAACTTATTTCTATACACTCAACAGCTCAACTTTGGGTAT 900
DB 841 TAGCGGCTTATCAACCGGTAACTTATTTCTATACACTCAACAGCTCAACTTTGGGTAT 900
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DB 841 TAGCGGCTTATCAACCGGTAACTTATTTCTATACACTCAACAGCTCAACTTTGGGTAT 900
QY 901 ACAGATTAATCTATCTTACGTGCGGAACCTTAATATATAGTGCGCACTTATTTGAAAC 960
DB 901 ACAGATTAATCTATCTTACGTGCGGAACCTTAATATATAGTGCGCACTTATTTGAAAC 960
QY 961 CTATTCGGTAAAGCAACACAGGGGATTTGCTCGGCACTTTGCCAAAAGTGTGACACA 1020
DB 961 CTATTCGGTAAAGCAACACAGGGGATTTGCTCGGCACTTTGCCAAAAGTGTGACACA 1020
QY 1021 GGTGGTTCGTGTATGAAGAAGCTTGACCTCTCATCTGTATGAAGAACTGATAGATT 1080
DB 1021 GGTGGTTCGTGTATGAAGAAGCTTGACCTCTCATCTGTATGAAGAACTGATAGATT 1080
QY 1081 ATATTGTACAAGATATGAAGTTCCTATATGTCCTCGTATTTATTCCTGCTTGACCGG 1140
DB 1081 ATATTGTACAAGATATGAAGTTCCTATATGTCCTCGTATTTATTCCTGCTTGACCGG 1140
QY 1141 CAATACGTGGCTGTATGTATCTCAANAGACCGAAGCGCACTTATCAACCATATCATGAC 1200
DB 1141 CAATACGTGGCTGTATGTATCTCAANAGACCGAAGCGCACTTATCAACCATATCATGAC 1200
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DB 1201 TATCAAAAGTTCACTCATTCGCAACCTGCAAGATGACAAACATGTATGTATTAACCCGCC 1260
QY 1261 GGGTATCATATTCGCAAACTATGAGAGAGCGGTCTCTATATAGATTAACAATCATGCA 1320
DB 1261 GGGTATCATATTCGCAAACTATGAGAGAGCGGTCTCTATATAGATTAACAATCATGCA 1320
QY 1321 TGTTTATCTTATAGCGGGATTAACCTTTAAGCTCAGTGGGAAATTCATGTAACTTATCA 1380
DB 1321 TGTTTATCTTATAGCGGGATTAACCTTTAAGCTCAGTGGGAAATTCATGTAACTTATCA 1380
QY 1381 GAAGAAATATCTCAATTAACAATCTCAAGTAAATTAACAAGCAATTTGATATCTCAAC 1440
DB 1381 GAAGAAATATCTCAATTAACAATCTCAAGTAAATTAACAAGCAATTTGATATCTCAAC 1440
QY 1441 TGAGCTTGGGAATGTCAACAACCTGATCAGTAAATGCTTTGAATATAGTAAAGAAACAA 1500
DB 1441 TGAGCTTGGGAATGTCAACAACCTGATCAGTAAATGCTTTGAATATAGTAAAGAAACAA 1500
QY 1501 CAGAAAATAGACCAAACTGATGCAATGCAATGCAATGCAATGCTCTCATTAATAT 1560
DB 1501 CAGAAAATAGACCAAACTGATGCAATGCAATGCAATGCAATGCTCTCATTAATAT 1560
QY 1561 CGTTTGTACATCATATCTCTGTTTGGTATTAATTAAGCTGATTTACAGAGCTACCT 1620
DB 1561 CGTTTGTACATCATATCTCTGTTTGGTATTAATTAAGCTGATTTACAGAGCTACCT 1620
QY 1621 AATGTACAAACAAAGGCGCAACAAACCTTATTAATGCTTGGAAATTAATCTAGA 1680
DB 1621 AATGTACAAACAAAGGCGCAACAAACCTTATTAATGCTTGGAAATTAATCTAGA 1680
QY 1681 TCAAGTGAAGCACTTACAAAAAATGTGAACACAGATGAGGACGAAGGTTTCCCTAATAG 1740
DB 1681 TCAAGTGAAGCACTTACAAAAAATGTGAACACAGATGAGGACGAAGGTTTCCCTAATAG 1740
QY 1741 TAATTTGTGAAGAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAAATCAACGGT 1800
DB 1741 TAATTTGTGAAGAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAAAATCAACGGT 1800
QY 1801 TGTATATGACCAAAAGGAGATATACGGGTGAAACGGTAAAGAGAGCGCCCTCAATTGC 1860
DB 1801 TGTATATGACCAAAAGGAGATATACGGGTGAAACGGTAAAGAGAGCGCCCTCAATTGC 1860
QY 1861 GAGCGAGGCTTCAACAACCTCGTTTCAACCGCTTCAACGACCAACAGTCTCAATCATAGAC 1920
DB 1861 GAGCGAGGCTTCAACAACCTCGTTTCAACCGCTTCAACGACCAACAGTCTCAATCATAGAC 1920
QY 1921 CGGCGCTTATGCAAGTGTGCTTAAGAGATGATGAAGAGAGCAAAAATTAATATGCGCG 1980
DB 1921 CGGCGCTTATGCAAGTGTGCTTAAGAGATGATGAAGAGAGCAAAAATTAATATGCGCG 1980
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Qy	1991	TTGATATTCGGGATTTGCAATCTTATTTCTTAACAGTAGAGCACTGGGCTATATCTGTAGCC	2040
Dp	1981	TTGATATTCGGGATTTGCAATCTTATTTCTTAACAGTAGAGCACTGGGCTATATCTGTAGCC	2040
Qy	2041	TTCCCTTTATATAGCATGGGGGCTTAGCAACACTAGCGATCTTGTAGGCATACGACTAGG	2100
Dp	2041	TTCCCTTTATATAGCATGGGGGCTTAGCAACACTAGCGATCTTGTAGGCATACGACTAGG	2100
Qy	2101	ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTAGTAT	2160
Dp	2101	ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTAGTAT	2160
Qy	2161	AGGATATATAGCAAGTGGCCCTTAGTGCTCCGTTGGCATGTGTAAATCTAGACCA	2220
Dp	2161	AGGATATATAGCAAGTGGCCCTTAGTGCTCCGTTGGCATGTGTAAATCTAGACCA	2220
Qy	2221	ATTATGAAACGAATPAACATCTCTCTCTATCAGATTATATGAGAGCTGCMAAACAGTGGG	2280
Dp	2221	ATTATGAAACGAATPAACATCTCTCTCTATCAGATTATATGAGAGCTGCMAAACAGTGGG	2280
Qy	2281	TGGGGGGGCACCTATCCATGACCAGATTATATAGGGGGGATAGGCAAGAACTCATGTGA	2340
Dp	2281	TGGGGGGGCACCTATCCATGACCAGATTATATAGGGGGGATAGGCAAGAACTCATGTGA	2340
Qy	2341	GATGATGCTAGTATGATGATCAATCATTTATCCCTCTGCAATTTCAAGAACATCTGAATTT	2400
Dp	2341	GATGATGCTAGTATGATGATCAATCATTTATCCCTCTGCAATTTCAAGAACATCTGAATTT	2400
Qy	2401	ATCCCGGGGCTACTACAGAGATACGGTTGCACTGGAATACCTCATTTGACATGAGTCT	2460
Dp	2401	ATCCCGGGGCTACTACAGAGATACGGTTGCACTGGAATACCTCATTTGACATGAGTCT	2460
Qy	2461	ACCATTATCTGCTACACCCATATATGTATTTGTCTGATGCAGAGATCACTGCATATTCA	2520
Dp	2461	ACCATTATCTGCTACACCCATATATGTATTTGTCTGATGCAGAGATCACTGCATATTCA	2520
Qy	2521	TATCAGTATTTTAGCACTTGTGTGTCTCCGACATCTGCACAACGAGGAGGTTATCTTTTCT	2580
Dp	2521	TATCAGTATTTTAGCACTTGTGTGTCTCCGACATCTGCACAACGAGGAGGTTATCTTTTCT	2580
Qy	2581	ACTCTGCGTTCCATCTAACCTTGGACGACACCCAAAATCGGAAGTCTTGGAGGTGATGCA	2640
Dp	2581	ACTCTGCGTTCCATCTAACCTTGGACGACACCCAAAATCGGAAGTCTTGGAGGTGATGCA	2640
Qy	2641	ACTCCCGGGGTTGTGATGTGTGTGCTGCAAAAGTCAAGAGACAGAGAAAGAAATAT	2700
Dp	2641	ACTCCCGGGGTTGTGATGTGTGTGCTGCAAAAGTCAAGAGACAGAGAAAGAAATAT	2700
Qy	2701	AACCTCAGCTGTCCCTTACCGCGATGGTACATGGAGGTTAGGGTTTCAGCGGCCAGTACAC	2760
Dp	2701	AACCTCAGCTGTCCCTTACCGCGATGGTACATGGAGGTTAGGGTTTCAGCGGCCAGTACAC	2760
Qy	2761	GAAGAAAGCACTAGATGTCAACAATTATTCGGGGACTGGGTGGCCMACTACCCAGAGATGA	2820
Dp	2761	GAAGAAAGCACTAGATGTCAACAATTATTCGGGGACTGGGTGGCCMACTACCCAGAGATGA	2820
Qy	2821	GGGGGTGATCTTTTATTTAGCAGCCGCGGTATGTCTCAGTCTACAGAGGGGTTAAACCC	2880
Dp	2821	GGGGGTGATCTTTTATTTAGCAGCCGCGGTATGTCTCAGTCTACAGAGGGGTTAAACCC	2880
Qy	2881	AATTCAACCAAGTCACTGTACAGAGAAAGGAAATATGTGATATACACGATACATATGAC	2940
Dp	2881	AATTCAACCAAGTCACTGTACAGAGAAAGGAAATATGTGATATACACGATACATATGAC	2940
Qy	2941	ACATGCCAGATGACCAAGACTACCAAGATTCGAATGGCCAAAGTCTTCTGATATAGCTTGA	3000
Dp	2941	ACATGCCAGATGACCAAGACTACCAAGATTCGAATGGCCAAAGTCTTCTGATATAGCTTGA	3000
Qy	3001	CGGTTTGGTGGAAACGATACAGAGGCTATCTTATATCAAGAGTGTCAACATCTCTTA	3060
Dp	3001	CGGTTTGGTGGAAACGATACAGAGGCTATCTTATATCAAGAGTGTCAACATCTCTTA	3060

Accession	Species	Gene	Location/Qualifiers
QY	GGGCAAGACCCCGGACTGACGTACCGGCCCAACACAGTCACATCAGGGGCGGAAGGC	3120	
Db	GGGCAAGACCCCGGACTGACGTACCGGCCCAACACAGTCACATCAGGGGCGGAAGGC	3120	
QY	AGAAATTCACAGTAGGAGACATCTCATTTCTTGATCAACAGAGGATCATCTTCTCT	3180	
Db	AGAAATTCACAGTAGGAGACATCTCATTTCTTGATCAACAGAGGATCATCTTCTCT	3180	
QY	CCCGCGTTATTATATTCCTATGACAGTCAGCAACAAAACAGCACTCTTCATATGTCCTTAT	3240	
Db	CCCGCGTTATTATATTCCTATGACAGTCAGCAACAAAACAGCACTCTTCATATGTCCTTAT	3240	
QY	ACATTCATAGGCTTCACCTCGGCGCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC	3300	
Db	ACATTCATAGGCTTCACCTCGGCGCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC	3300	
QY	AACCTGCTGTGTACTGAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358	
Db	AACCTGCTGTGTACTGAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358	
RESULT 2			
AAZ44617	AAZ44617	standard; DNA; 15186 BP.	
XX	AAZ44617;		
AC			
DT	07-APR-2000 (first entry)		
XX			
DE	Newcastle disease virus LaSota genomic DNA.		
XX			
KW	Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;		
KM	respiratory disease; gastrointestinal disease; poultry pathogen;		
KW	local immunity; ds.		
XX			
OS	Newcastle disease virus.		
XX			
PH	Key	Location/Qualifiers	
FT	122..1591		
FT	/*tag= a		
FT	1887..3074		
FT	/*tag= b		
FT	3290..4384		
FT	/*tag= c		
FT	4544..6205		
FT	/*tag= d		
FT	6412..8145		
FT	/*tag= e		
FT	8381..14995		
FT	/*tag= f		
XX			
PN	W09966045-A1.		
XX			
PD	23-DEC-1999.		
XX			
PF	17-JUN-1999; 99WO-NL000377.		
XX			
PR	19-JUN-1998; 98EP-00202054.		
XX			
PA	(DIEN-) STICHTING DIENST LANDEBOLKUNDIG ONDERZOE.		
XX			
PI	Peeters BPB, De Leeuw OS, Koch G, Gielkens ALJ;		
XX			
DR	WPI; 2000-106102/09.		
XX			
XX	New avian paramyxovirus cDNA, useful for production of vaccine against		
PT	Newcastle disease virus.		
XX			
PS	Disclosure; Fig 3; 115pp; English.		
XX			
CC	This invention describes a novel avian-paramyxovirus cDNA (I) which		
CC	comprises a nucleic acid sequence corresponding to the 5' terminal end of		



CC infectious copy of avian paramyxovirus. The cell line is useful for the  
CC production of infectious lentogenic NDV (Newcastle Disease virus) without  
CC the addition of exogenous proteolytic activity. Also it is possible to  
CC generate a stable transfected cell line that expresses the wild-type F  
CC protein in the virus envelope therefore providing infectious particles,  
CC useful in the form of a vaccine, especially against respiratory and/or  
CC gastrointestinal diseases. NDV can be easily cultured to very high titers  
CC in embryonated eggs. Mass culture of embryonated eggs is relatively  
CC cheap. NDV vaccines are relatively stable and can be simply administered  
CC by mass application methods e.g. drinking water or by spraying or by  
CC aerosol formation. The natural route of infection is by the respiratory  
CC and/or gastrointestinal tract which are also the major routes of  
CC infection of many other poultry pathogens. NDV can induce local immunity  
CC despite the presence of circulating maternal antibody. This sequence  
CC represents the NDV strain lasota genome DNA  
CC  
XX  
SQ Sequence 15186 BP; 4431 A; 3544 C; 3462 G; 3749 T; 0 U; 0 Other;  
Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
DB 4498 ACGGGTGAAGATTCTGGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557  
QY 61 TTTCACCAAGAACCCAGACCTATGATGCTGATATCCGGGTTTCGGTGGCATGAGTTG 120  
DB 4558 TTTCACCAAGAACCCAGACCTATGATGCTGATATCCGGGTTTCGGTGGCATGAGTTG 4617  
QY 121 CATCTGTCGGGCAAACTTCATTTGATGGAGCCCTTTCGACGTGCAAGAAATTTGGTTAC 180  
DB 4618 CATCTGTCGGGCAAACTTCATTTGATGGAGCCCTTTCGACGTGCAAGAAATTTGGTTAC 4677  
QY 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAAGT 240  
DB 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAAGT 4737  
QY 241 CCTCCCAATCTGCCCAGATGAAGAGCATGTGCGAAAGCCCTTCGTGATGATCAAA 300  
DB 4738 CCTCCCAATCTGCCCAGATGAAGAGCATGTGCGAAAGCCCTTCGTGATGATCAAA 4797  
QY 301 CAGGACATTGACCATTTTGTCTCACCCCTTGTGATCTTATCCGTAGATCAAGAGTC 360  
DB 4798 CAGGACATTGACCATTTTGTCTCACCCCTTGTGATCTTATCCGTAGATCAAGAGTC 4857  
QY 361 TGTGACATCAATCTGGAGGGGGGAGACAGGGGGCCCTTATGAGGGCCCTTATTTGGCGGTG 420  
DB 4858 TGTGACATCAATCTGGAGGGGGGAGACAGGGGGCCCTTATGAGGGCCCTTATTTGGCGGTG 4917  
QY 421 GGGCTTTGGGGTTGCAATCGCCGACAAATTAACAGCGCGCAGCTGTGATCAAGCCAA 480  
DB 4918 GGGCTTTGGGGTTGCAATCGCCGACAAATTAACAGCGCGCAGCTGTGATCAAGCCAA 4977  
QY 481 ACAAAATGCTGCCAATCTCTCGACTTAAAGAGAGCATTTGCCGAACAATGAGCTGT 540  
DB 4978 ACAAAATGCTGCCAATCTCTCGACTTAAAGAGAGCATTTGCCGAACAATGAGCTGT 5037  
QY 541 GCATGAGGTGACTGACGGATTATGCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 600  
DB 5038 GCATGAGGTGACTGACGGATTATGCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 5097  
QY 601 TGTTAATGACCAATTTAATAAAACAGCTCAGAAATTAAGACTGATCAAAATTTGCACGCA 660  
DB 5098 TGTTAATGACCAATTTAATAAAACAGCTCAGAAATTAAGACTGATCAAAATTTGCACGCA 5157  
QY 661 AGTTGTGTAAGCTCAACCTGTACCTAACCGAAATTAAGTCAAGTATTTGGACCACAAT 720  
DB 5158 AGTTGTGTAAGCTCAACCTGTACCTAACCGAAATTAAGTCAAGTATTTGGACCACAAT 5217  
QY 721 CACTTACCTGCTTTAAACAAGCTGATATTCAAGGCACTTTAACAATCTAGCTGGTGA 780  
DB 5218 CACTTACCTGCTTTAAACAAGCTGATATTCAAGGCACTTTAACAATCTAGCTGGTGA 5277

QY 781 TATGATTAATCTTATTTGATCTAAGTTAGTGAAGAAACAATCACTCAAGCTTAAATCGG 840  
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QY 841 TAGCGGCTTAATCAACCGGTAAACCTTATTTAGTCACTCAAGCTCAAGCTTGGGTAT 900  
DB 5338 TAGCGGCTTAATCAACCGGTAAACCTTATTTAGTCACTCAAGCTCAAGCTTGGGTAT 5397  
QY 901 ACAGTAATCTAATCTTCACTGCGGAACCTTAATATATATGCTGCGCACTTATTTGAAC 960  
DB 5398 ACAGTAATCTAATCTTCACTGCGGAACCTTAATATATATGCTGCGCACTTATTTGAAC 5457  
QY 961 CTTATCCGTAGCAACAACGGGATTTGCTTGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTAGCAACAACGGGATTTGCTTGGCACTTGTCCCAAAAGTGTGACACA 5517  
QY 1021 GGTCCGTTCTGTATTAAGAAACCTTGACACTGATATCTGATTAAGAACTGATTAAGTTT 1080  
DB 5518 GGTCCGTTCTGTATTAAGAAACCTTGACACTGATATCTGATTAAGAACTGATTAAGTTT 5577  
QY 1081 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCTGATTTATTTCTGCTTGAACGG 1140  
DB 5578 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCTGATTTATTTCTGCTTGAACGG 5637  
QY 1141 CAATACGTGGCTGTATTTGATCTCAAAAGACCGAAGCGCACTTATACCATTCATGAC 1200  
DB 5638 CAATACGTGGCTGTATTTGATCTCAAAAGACCGAAGCGCACTTATACCATTCATGAC 5697  
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DB 5698 TATCAAAAGTTCACTGATGCGCAACTGCAAGATGACAAACATGTAAGTGTAAACCCCGC 5757  
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DB 5818 TGTTTTATCTTATAGCGGGATTAACCTTAAAGCTCAAGTGGGAATTCGATGTAATTCA 5877  
QY 1381 GAGGAATATCTCAATTCAGAAATTCAGAAATTAATTAACAGGCAATTTGATATCTCAAC 1440  
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DB 5998 CAGAAAATTAAGCAAAAGTCAATGTCAAACTGACTAGACATCTGCTCATTAATAT 6057  
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DB 6058 CGTTTGTGACTATCATATCTCTGTTTGTGTAATCACTTAAGCTTAATTAAGTCACTA 6117  
QY 1621 AATGTACAAGCAAAAGCGGCAAAACCTTATTAATGCTTGGGAATTAATCTCTAGA 1680  
DB 6118 AATGTACAAGCAAAAGCGGCAAAACCTTATTAATGCTTGGGAATTAATCTCTAGA 6177  
QY 1681 TCAGATGAGACCACTACAAAATTTGTAACACAGATGAGGAACGAAGTTTCCCTAATAG 1740  
DB 6178 TCAGATGAGACCACTACAAAATTTGTAACACAGATGAGGAACGAAGTTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAAGTTCTGTGTGTCTGTAGTTCAGAGTTTAAGAAAAAATCAACGGT 1800  
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QY 1801 TGTAGATGACCAAAAGGACGATATACGGGTGGAACGGTTAAGAGAGCGCCCTCAATTGC 1860  
DB 6298 TGTAGATGACCAAAAGGACGATATACGGGTGGAACGGTTAAGAGAGCGCCCTCAATTGC 6357

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QY 1861 GAGCCAGGCTTCACAACTCCGTTCTACCGCTTACCGGACAAAGTCTCAATCATGAGAC 1920
Db 6358 GAGCCAGGCTTCACAACTCCGTTCTACCGCTTACCGGACAAAGTCTCAATCATGAGAC 6417
QY 1921 CGCGCCCTTGGCCAGGTTGCGTTAGAGATGATGAAAAGAGGCAAAAATACATGAGGC 1980
Db 6418 CGCGCCCTTGGCCAGGTTGCGTTAGAGATGATGAAAAGAGGCAAAAATACATGAGGC 6477
QY 1981 TTGATATTCGGGATTCGAACTTATTTCTTAAACAGTAGTGAACCTTGGCTATATCTGAGCC 2040
Db 6478 TTGATATTCGGGATTCGAACTTATTTCTTAAACAGTAGTGAACCTTGGCTATATCTGAGCC 6537
QY 2041 TCCCTTTATATATAGCATGAGGAGCTAGCAACCTTAGCCATCTTGTAGGCAATACCACTAGG 2100
Db 6538 TCCCTTTATATATAGCATGAGGAGCTAGCAACCTTAGCCATCTTGTAGGCAATACCACTAGG 6597
QY 2101 ATTTCCAGGCGAAGAAAGAAATTAATCATCTACCTTGGTTCCATCAAGATGTAGTAAAT 2160
Db 6598 ATTTCCAGGCGAAGAAAGAAATTAATCATCTACCTTGGTTCCATCAAGATGTAGTAAAT 6657
QY 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATGTTAAATATGAGACACA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATGTTAAATATGAGACACA 6717
QY 2221 ATTATGAACGCAATTAACATCTCTCTTATCAGATTAAATGAGCTCAACAAACAGTGGG 2280
Db 6718 ATTATGAACGCAATTAACATCTCTCTTATCAGATTAAATGAGCTCAACAAACAGTGGG 6777
QY 2281 TGGGGGGGCACTTATTCATGACCCAGATTATATAGGGGGGATAGGCAAACTCATTTGTA 2340
Db 6778 TGGGGGGGCACTTATTCATGACCCAGATTATATAGGGGGGATAGGCAAACTCATTTGTA 6837
QY 2341 GATGATGTAGTGAATGTCATATTCATCCCTCTGCAATTCGAAGAACTGTGAATTTT 2400
Db 6838 GATGATGTAGTGAATGTCATATTCATCCCTCTGCAATTCGAAGAACTGTGAATTTT 6897
QY 2401 ATCCCGGCGCTTACTACAGATCAGTTCGACTCGAATACCTCATTTTGAACATGAGTCT 2460
Db 6898 ATCCCGGCGCTTACTACAGATCAGTTCGACTCGAATACCTCATTTTGAACATGAGTCT 6957
QY 2461 ACCCATTACTGCTACACCCATTAATGTATATTTGTGATGACAGATCACTCACTTCA 2520
Db 6958 ACCCATTACTGCTACACCCATTAATGTATATTTGTGATGACAGATCACTCACTTCA 7017
QY 2521 TATCAGATTATTAAGCACTGTGTGTGTCGCGAATCTGCAACAGGGAGGATTTCTTCT 2580
Db 7018 TATCAGATTATTAAGCACTGTGTGTGTCGCGAATCTGCAACAGGGAGGATTTCTTCT 7077
QY 2581 ACTCTGCGTTCCATCAACCTGGAACGACCAAAAATCGGAAGTCTTGGAGTGTAGTCA 2640
Db 7078 ACTCTGCGTTCCATCAACCTGGAACGACCAAAAATCGGAAGTCTTGGAGTGTAGTCA 7137
QY 2641 ACTCCCTGCGTGTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGAAATTAAT 2700
Db 7138 ACTCCCTGCGTGTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGAAATTAAT 7197
QY 2701 AACTCAGCTGTCCCTACCGCGGATGTATATGAGAGGTTAGGTTGAGGCGACAGTACAC 2760
Db 7198 AACTCAGCTGTCCCTACCGCGGATGTATATGAGAGGTTAGGTTGAGGCGACAGTACAC 7257
QY 2761 GAAAAGGACCTAGATGTACAAACATTATTCGGGGGCTGGGTGGCCAACTACCCAGAGATA 2820
Db 7258 GAAAAGGACCTAGATGTACAAACATTATTCGGGGGCTGGGTGGCCAACTACCCAGAGATA 7317
QY 2821 GGGGGGTGATCTTTTATTTAGACGCGCGGTATGTTCTCAGTCTACGAGGGGTTAAACCC 2880
Db 7318 GGGGGGTGATCTTTTATTTAGACGCGCGGTATGTTCTCAGTCTACGAGGGGTTAAACCC 7377
QY 2881 AATTCAACCACTGACACTGTACAGAGAGGAAATATGATATTAACCGATACATGATAC 2940
Db 7378 AATTCAACCACTGACACTGTACAGAGAGGAAATATGATATTAACCGATACATGATAC 7437
QY 2941 ACATGCCCAAGATGAGCAAGACTACAGATTCGAATGCGCAAGTCTTCTATTAAGCTGGA 3000
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Db 7438 ACATGCCCAAGATGAGCAAGACTACCAAGTTGGAATGGCCAAAGTCTTGTATTAAGCTGGA 7497
QY 3001 CGGTTTGGTGGGAAACCATACAGACAGGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060
Db 7498 CGGTTTGGTGGGAAACCATACAGACAGGCTATCTTATCTATCAAGTGTCAACATCTTTA 7557
QY 3061 GGGCAAGACCCGGTACTGACTGTATCCGCCCAACACAGTCAACCTCATAGGGGGCCGAAGGC 3120
Db 7558 GGGCAAGACCCGGTACTGACTGTATCCGCCCAACACAGTCAACCTCATAGGGGGCCGAAGGC 7617
QY 3121 AGAATTCACAGTAGGGAACATCTCATTTCTGTATCAAGAGGGATCATACTCTCT 3180
Db 7618 AGAATTCACAGTAGGGAACATCTCATTTCTGTATCAAGAGGGATCATACTCTCT 7677
QY 3181 CCCGCTTATATATATCTTATGACAGTGAAGCAACAAAACAGCACTTTCATATGCTTAT 3240
Db 7678 CCCGCTTATATATATCTTATGACAGTGAAGCAACAAAACAGCACTTTCATATGCTTAT 7727
QY 3241 ACATTCATGCTTACTGAGTGTATATACAGATTCATATCCCTTAATCTTATAGAAAC 3300
Db 7728 ACATTCATGCTTACTGAGTGTATATACAGATTCATATCCCTTAATCTTATAGAAAC 7797
QY 3301 AACTCGTGTCTTACTGAGTGTATATACAGATTCATATCCCTTAATCTTATAGAAAC 3358
Db 7798 AACTCGTGTCTTACTGAGTGTATATACAGATTCATATCCCTTAATCTTATAGAAAC 7855

RESULT 3
ADH71088
ID ADH71088 standard; DNA; 15186 BP.
XX
AC ADH71088;
XX
DT 25-MAR-2004 (first entry)
XX
DE Newcastle disease virus HN gene.
XX
XX Virulence; vaccine accelerator factor; VAF; immuno-stimulant;
XX infectious bronchitis virus; IBV; Newcastle disease virus; NDV;
XX infectious bursal disease virus; IBDV; Newcastle disease virus; NDV;
XX infectious bronchitis virus; IBV; fowlpox virus; FPV;
XX infectious laryngotracheitis virus; ILTV; avian encephalomyelitis virus;
XX AEV; avian leukosis virus; ALV; avian parainfluenza virus; APV;
XX duck hepatitis virus; DHV; hemorrhagic enteritis virus; HEV; HN; ds.
XX
OS Newcastle disease virus.
XX
XX US2003207836-A1.
XX
XX 06-NOV-2003.
XX
XX 06-MAY-2003; 2003US-00429735.
XX
XX 08-MAR-2002; 2002US-0362547P.
XX
XX 04-MAR-2003; 2003US-00377718.
XX
XX (KUOT/) KUO T Y.
XX
XX Kuo TY;
XX
XX WPI, 2003-875897/81.
XX
XX New vaccine accelerator factor (VAF) comprising one or more DNA
XX constructs, each comprising a DNA molecule and a vector, useful as a
XX vaccine for viruses that affect chicken.
XX
XX Claim 13; SEQ ID NO 3; 28bp; English.
XX
XX The present invention provides a vaccine accelerator factor (VAF) which
XX is an in ovo nucleoclide immuno-stimulant. The VAF comprises one or more
XX DNA constructs, each comprising a DNA molecule and a vector, where each
XX of the DNA molecule contains one or more genes or gene fragments each
```

CC encoding an antigenic peptide of an avian virus. VAF accelerates and  
CC stimulates a protective immune response of a viral vaccine against the  
CC avian virus. VAF is useful as a vaccine against Marek's disease virus  
CC (MDV), infectious bursal disease virus (IBDV), Newcastle disease virus  
CC (NDV), infectious bronchitis virus (IBV), fowlpox virus (FPV), infectious  
CC laryngotracheitis virus (ILT), avian encephalomyelitis virus (AEV),  
CC avian leukosis virus (ALV), avian parainfluenza virus (APV), duck  
CC hepatitis virus (DHV) and hemorrhagic enteritis virus (HEV) in chicken.  
CC The present sequence is NDV HN gene.  
XX

Sequence 15186 BP; 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ACGGGTGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTCGAAGATGGGCTCCAGACC 60
D 4498 ACGGGTGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTCGAAGATGGGCTCCAGACC 4557
QY 61 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGGCGCTGCACTGAGTTG 120
D 4558 TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGGCGCTGCACTGAGTTG 4617
QY 121 CATCTGTCGGCAAACTCATTTGATGCGAGCCCTCTTGCACTGCAAGATTGGTTAC 180
D 4618 CATCTGTCGGCAAACTCATTTGATGCGAGCCCTCTTGCACTGCAAGATTGGTTAC 4677
QY 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 240
D 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 4737
QY 241 CCTCCCAATCTGCCCAAGATTAAGAGCATGTGCGAAGGCCCTTGATGATCAAA 300
D 4738 CCTCCCAATCTGCCCAAGATTAAGAGCATGTGCGAAGGCCCTTGATGATCAAA 4797
QY 4798 CAGGACATTGACCACTTGTGCTCAACCCCTTGATGACTCTATCCGATGAGATCAAGATC 4857
D 4798 CAGGACATTGACCACTTGTGCTCAACCCCTTGATGACTCTATCCGATGAGATCAAGATC 4857
QY 361 TGTGACTACATCTGAGAGGGGGGAGACAGGGGGGCTTATAGGGCGCATTTATGGCGGTG 420
D 4858 TGTGACTACATCTGAGAGGGGGGAGACAGGGGGGCTTATAGGGCGCATTTATGGCGGTG 4917
QY 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCGCAGACTGTGATTAAGCCAA 480
D 4918 GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCGCAGACTGTGATTAAGCCAA 4977
QY 481 ACAAATGCTGCAACATCTCTCGCATTTAAAGAGCATTTGCGCAACCAATGAGGCTGT 540
D 4978 ACAAATGCTGCAACATCTCTCGCATTTAAAGAGCATTTGCGCAACCAATGAGGCTGT 5037
QY 541 GCATGAGGTGACATGACGATTTATGCAACTGACAGTGGCAGTTGGGAAGATGAGCAGTT 600
D 5038 GCATGAGGTGACATGACGATTTATGCAACTGACAGTGGCAGTTGGGAAGATGAGCAGTT 5097
QY 601 TGTATATGACCAATTTATATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 660
D 5098 TGTATATGACCAATTTATATAAAACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCA 5157
QY 661 AGTTGTGTGAGAGCTCAACCTGTACCTTAACCGAATTTGATCAAGATTTGGACCAAAAT 720
D 5158 AGTTGTGTGAGAGCTCAACCTGTACCTTAACCGAATTTGATCAAGATTTGGACCAAAAT 5217
QY 721 CACTTACCTGCTTTAAACAAAGCTGATTAAGGCACTTTAACAATCTAGTGGTGGAAA 780
D 5218 CACTTACCTGCTTTAAACAAAGCTGATTAAGGCACTTTAACAATCTAGTGGTGGAAA 5277
QY 781 TATGATTAATCTTATTTGATTAAGTTAGTTAGGGAACAATCAATCACTGATCAATTAATCG 840
D 5278 TATGATTAATCTTATTTGATTAAGTTAGTTAGGGAACAATCAATCACTGATCAATTAATCG 5337
QY 841 TAGCGGCTTAATCAACCGGTAAACCTTATTTATTAACGACTCAAGACTCAATCTTTGGGTAT 900
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D 5338 TAGCGGCTTAATCAACCGGTAAACCTTATTTATTAACGACTCAAGACTCAATCTTTGGGTAT 5397
QY 901 AAGAGTAATCTACCTTCAAGTCGGGAACCTTAATATATGCTGTCGCACTACTTGGAAAC 960
D 5398 AAGAGTAATCTACCTTCAAGTCGGGAACCTTAATATATGCTGTCGCACTACTTGGAAAC 5457
QY 961 CTATTCGGTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCGCCAAAGTGTGACACA 1020
D 5458 CTATTCGGTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCGCCAAAGTGTGACACA 5517
QY 1021 GGTGCTTGTGTGATGAAGAACTTGACACCTCATCTGTATGAACCTAGTAAATTT 1080
D 5518 GGTGCTTGTGTGATGAAGAACTTGACACCTCATCTGTATGAACCTAGTAAATTT 5577
QY 1081 ATATTGTACAAAGATTAAGTAAAGTTCCCTATATGCTCCCTGATTAATTAATCTGCTTGAACGG 1140
D 5578 ATATTGTACAAAGATTAAGTAAAGTTCCCTATATGCTCCCTGATTAATTAATCTGCTTGAACGG 5637
QY 1141 CAATACGTGGCCCTGATATGTAATCTCAAGACCGAAGGCGCATTAATCAACATATGATGAC 1200
D 5638 CAATACGTGGCCCTGATATGTAATCTCAAGACCGAAGGCGCATTAATCAACATATGATGAC 5697
QY 1201 TATCAAAAGTTCAATCATGCGCAACTGCAAGATGACAAACATGATGATGATTAACCCGCC 1260
D 5698 TATCAAAAGTTCAATCATGCGCAACTGCAAGATGACAAACATGATGATGATGATTAACCCGCC 5757
QY 1261 GGGTATCATATCGCAAACTATGAGAGAGCCGCTGCTCTAATAGATTAACATATGATCAAA 1320
D 5758 GGGTATCATATCGCAAACTATGAGAGAGCCGCTGCTCTAATAGATTAACATATGATCAAA 5817
QY 5818 TGTATTATCTTATAGGCGGATTAACCTTTAAGGCTCATGAGGGAATTCGATGTAACCTATCA 1380
D 1321 TGTATTATCTTATAGGCGGATTAACCTTTAAGGCTCATGAGGGAATTCGATGTAACCTATCA 1440
QY 1381 GAAGAAATATCTCAATTAACAATTTCTGAATTAATTAACAAGGAATTTGATATCTCAAC 1440
D 5878 GAAGAAATATCTCAATTAACAATTTCTGAATTAATTAACAAGGAATTTGATATCTCAAC 5937
QY 1441 TGAGCTTGGGAATGTCACAACTCGATCAATATGCTTTGAATTAAGTAAAGGAAAGCAA 1500
D 5938 TGAGCTTGGGAATGTCACAACTCGATCAATATGCTTTGAATTAAGTAAAGGAAAGCAA 5997
QY 1501 CAGAAAATGACAAAGTCAATGTCAAACTGACTAGACACATCTGCTCATTAATCTATAT 1560
D 5998 CAGAAAATGACAAAGTCAATGTCAAACTGACTAGACACATCTGCTCATTAATCTATAT 6057
QY 1561 CGTTTGTACATATATCTTGTGTTTGGTATATCTTAAGCTGATTTACATGCTACCT 1620
D 6058 CGTTTGTACATATATCTTGTGTTTGGTATATCTTAAGCTGATTTACATGCTACCT 6117
QY 1621 AATGTACAAAGCAAAAGCGGCAAAAACCTTATTATGCTTGGGAATTAATCTTACA 1680
D 6118 AATGTACAAAGCAAAAGCGGCAAAAACCTTATTATGCTTGGGAATTAATCTTACA 6177
QY 1681 TCAGATGAGCACTACAAAAAATGTGAACACAGATGAGGAAGCAAGGTTTCCCTAATAG 1740
D 6178 TCAGATGAGCACTACAAAAAATGTGAACACAGATGAGGAAGCAAGGTTTCCCTAATAG 6237
QY 1741 TAAATTTGTGAAAAGTTCTGCTATGCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 1800
D 6238 TAAATTTGTGAAAAGTTCTGCTATGCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 6297
QY 1801 TGTATGATGACCAAAAGGCGATATACGGGGTGAAGCGGTAAAGAGAGGCGCGCCCTCAATTGC 1860
D 6298 TGTATGATGACCAAAAGGCGATATACGGGGTGAAGCGGTAAAGAGAGGCGCGCCCTCAATTGC 6357
QY 1861 GAGCGAGGCTTCAACAACCTCCGTTCTACCGCTTCAACCGACCAACAGTCTCTCAATCATGAGAC 1920
D 6358 GAGCGAGGCTTCAACAACCTCCGTTCTACCGCTTCAACCGACCAACAGTCTCTCAATCATGAGAC 6417
QY 1921 CGCGCGCTTAAGCAAGTTGCGTTAAGATGATGAAGAGAGGCAAAAATACATGCGCG 1980
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D 6418 GCGCCGTTAGCCAAAGTTCCGTTAGAGATGATGAAAGAGAGCGCAAAAATACATGGCC 6477  
Q 1981 TTGATATTCGGATTCGAACTTATTTCTTAAAGATGACCTTGCTATATCTGAGCC 2040  
D 6478 TTGATATTCGGATTCGAACTTATTTCTTAAAGATGACCTTGCTATATCTGAGCC 6537  
Q 2041 TCCCTTTTATATGACATGAGGAGGCTAGACACCTAGCCGATCTTGAGGATACCGACTAGG 2100  
D 6538 TCCCTTTTATATGACATGAGGAGGCTAGACACCTAGCCGATCTTGAGGATACCGACTAGG 6597  
Q 2101 ATTTCCAGGGAGAGAAAGAAATTAACCTACCTAGGTTCCATCAAGATGATGAT 2160  
D 6598 ATTTCCAGGGAGAGAAAGAAATTAACCTACCTAGGTTCCATCAAGATGATGAT 6657  
Q 2161 AGATATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTAAATAGTGAACCA 2220  
D 6658 AGATATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTAAATAGTGAACCA 6717  
Q 2221 ATATGAAAGCAATPAACATCTCTCTCTTATCAGATTAATGAGCTGCMAACAGTGGG 2280  
D 6718 ATATGAAAGCAATPAACATCTCTCTCTTATCAGATTAATGAGCTGCMAACAGTGGG 6777  
Q 2281 TGGGGGCACTATCCATGACACCAATTAATAGGGGGGATAGCAAGAACTCATTTGTA 2340  
D 6778 TGGGGGCACTATCCATGACACCAATTAATAGGGGGGATAGCAAGAACTCATTTGTA 6837  
Q 2341 GATGATGCTAGTATGTCATCATCTCTCTCTGATTTCAAGAACTCTGAATTTT 2400  
D 6838 GATGATGCTAGTATGTCATCATCTCTCTCTGATTTCAAGAACTCTGAATTTT 6897  
Q 2401 ATCCCGGCGCTTACTACAGATCAGTTCGATCGAATACCTCATTTGACATGAGTCT 2460  
D 6898 ATCCCGGCGCTTACTACAGATCAGTTCGATCGAATACCTCATTTGACATGAGTCT 6957  
Q 2461 ACCCATTAAGTCTACACCCATTAATGTAATTTGCTGATGCAAGATCCTCATTTCA 2520  
D 6958 ACCCATTAAGTCTACACCCATTAATGTAATTTGCTGATGCAAGATCCTCATTTCA 7017  
Q 2521 TATCAGATTTAGACATGCTGCTGCTCGGACATCTGCAACAGGGAGGTTATCTTTCT 2580  
D 7018 TATCAGATTTAGACATGCTGCTGCTCGGACATCTGCAACAGGGAGGTTATCTTTCT 7077  
Q 2581 ACTCTGGGTTTCATCAACCTGAGACACCCAAATCGAAGTCTTGACGTGAGTGA 2640  
D 7078 ACTCTGGGTTTCATCAACCTGAGACACCCAAATCGAAGTCTTGACGTGAGTGA 7137  
Q 2641 ACTCTGGGTTGATATGCTGCTGCAAGTCTGACGAGACAGAGAAAGATTTAT 2700  
D 7138 ACTCTGGGTTGATATGCTGCTGCAAGTCTGACGAGACAGAGAAAGATTTAT 7197  
Q 2701 AACTCAGCTGCTTACCGGAGTGGTACATGAGGTTAGGGTTGACGCGCAGTACAC 2760  
D 7198 AACTCAGCTGCTTACCGGAGTGGTACATGAGGTTAGGGTTGACGCGCAGTACAC 7257  
Q 2761 GAAAGAGACCTAGATGTCACAACATTTATCGGAGCTGAGTGCACATACCCAGAGTA 2820  
D 7258 GAAAGAGACCTAGATGTCACAACATTTATCGGAGCTGAGTGCACATACCCAGAGTA 7317  
Q 2821 GGGGGTGGATCTTTTATTTAGACGCGCGCTATGTTCTCAGTCTACGAGGGTTAAACC 2880  
D 7318 GGGGGTGGATCTTTTATTTAGACGCGCGCTATGTTCTCAGTCTACGAGGGTTAAACC 7377  
Q 2881 AATTCAACCACTGACCTGTACAGAAAGGAAATATGTAATATCAACCGATTAACATAC 2940  
D 7378 AATTCAACCACTGACCTGTACAGAAAGGAAATATGTAATATCAACCGATTAACATAC 7437  
Q 2941 ACATGCCAGATGACAGACTACAGATGCAATGCGCAAGTCTTCTATAGGCTTGA 3000  
D 7438 ACATGCCAGATGACAGACTACAGATGCAATGCGCAAGTCTTCTATAGGCTTGA 7497  
Q 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAGGTCTCAACATCCTTA 3060  
D 7498 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAGGTCTCAACATCCTTA 7557

Q 3061 GCGAAGACCCGCTAGTACTGTATCCGCCAACACAGTCACTCATATGCGGGCCGAAGGC 3120  
D 7558 GCGAAGACCCGCTAGTACTGTATCCGCCAACACAGTCACTCATATGCGGGCCGAAGGC 7617  
Q 3121 AGATTTCTACAGAGGAGACATCTCTGTTGATGACGAGGGGTATCATCTTCTCT 3180  
D 7618 AGATTTCTACAGAGGAGACATCTCTGTTGATGACGAGGGGTATCATCTTCTCT 7677  
Q 3181 CCCCGTTATATATCTTATGACAGTACAGCAACAAACAGCACTCTCATATGCTTAT 3240  
D 7678 CCCCGTTATATATCTTATGACAGTACAGCAACAAACAGCACTCTCATATGCTTAT 7737  
Q 3241 ACATTCATGCTTACTGAGTCTAGTATCCCTTGCCAGGCTTACAGCAAGTCCCC 3300  
D 7738 ACATTCATGCTTACTGAGTCTAGTATCCCTTGCCAGGCTTACAGCAAGTCCCC 7797  
Q 3301 AACTCGTGTATCTAGAGTCTATACAGTCCATATCCCTTAATCTTATAGAAAC 3358  
D 7798 AACTCGTGTATCTAGAGTCTATACAGTCCATATCCCTTAATCTTATAGAAAC 7855

## RESULT 4

ADH62844 ID ADH62844 standard; DNA, 15186 BP.

XX ADH62844;

XX 25-MAR-2004 (first entry)

XX Newcastle disease virus (NDV) HN gene.

XX Multivalent DNA vaccine; ovo injection; avian viral disease; fowl;

XX immune response; gene; Newcastle disease virus; NDV;

XX haemagglutinin neuraminidase; ds; HN.

XX Newcastle disease virus.

XX US2003175291-A1.

XX 18-SEP-2003.

XX 04-MAR-2003; 2003US-00377718.

XX 08-MAR-2002; 2002US-0362547P.

XX (KUOT/) KUO T Y.

XX Kuo TY;

XX WPI; 2003-898502/82.

XX Multiple DNA vaccine for in ovo injection, useful for inducing protective

XX immune response against the avian viral diseases in fowl, comprises two

XX or more DNA constructs.

XX Claim 10; SEQ ID NO 3; 26pp; English.

XX The invention relates to multiple and multivalent DNA vaccine for in ovo

XX injection which comprises two or more DNA constructs, where each DNA

XX construct expresses an antigenic protein of an avian virus causing avian

XX viral disease in fowl. The antigenic protein of the avian virus is

XX capable of inducing a protective immune response against the avian viral

XX disease in the fowl. The vaccine is useful for inducing protective immune

XX response against the avian viral diseases in fowl. The present sequence

XX is Newcastle disease virus (NDV) haemagglutinin neuraminidase (HN) gene

XX used in multiple and multivalent DNA vaccine.

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCGAGGTGCAAGATGGGCTTCAGACC 60  
Db 4498 ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCGAGGTGCAAGATGGGCTTCAGACC 4557  
Qy 61 TTCTACCAAGAACCCAGACCTTATGATGTGACTATCCGGGTTGGCTGGCACTGAATTG 120  
Db 4558 TTCTACCAAGAACCCAGACCTTATGATGTGACTATCCGGGTTGGCTGGCACTGAATTG 4617  
Qy 121 CATGTGCGGCAAACTCCATGTATGGCAGGCTCTTGAGCTCAGAAATTTGTGTAC 180  
Db 4618 CATGTGCGGCAAACTCCATGTATGGCAGGCTCTTGAGCTCAGAAATTTGTGTAC 4677  
Qy 181 AGGAGCAAAAGCCGTCACAATATACCTCATCCAGACAGATCAATCATAGTTAAAGT 240  
Db 4678 AGGAGCAAAAGCCGTCACAATATACCTCATCCAGACAGATCAATCATAGTTAAAGT 4737  
Qy 241 CTTCCCAATCTGCGCAAGATTAGAGGCAATGTCGCAAAAGCCCTTGATGATCA 300  
Db 4738 CTTCCCAATCTGCGCAAGATTAGAGGCAATGTCGCAAAAGCCCTTGATGATCA 4797  
Qy 301 CAGGACATGACCACTTGTGCAACCCCTTGATGATCACTGATGAGATCAAGAGTC 360  
Db 4798 CAGGACATGACCACTTGTGCAACCCCTTGATGATCACTGATGAGATCAAGAGTC 4857  
Qy 361 TGTGACTACATCTGAGAGGGGAGACAGGGCGCCTTATAGCGCCATTTATGGCGGTG 420  
Db 4858 TGTGACTACATCTGAGAGGGGAGACAGGGCGCCTTATAGCGCCATTTATGGCGGTG 4917  
Qy 421 GGCTCTTGGGGTGCACCTGCGCAAAATACAGCGCGCGAGCTCTGATCAAGCCAA 480  
Db 4918 GGCTCTTGGGGTGCACCTGCGCAAAATACAGCGCGCGAGCTCTGATCAAGCCAA 4977  
Qy 481 ACAAAATGCTGCCAACATCCCTCGACTTAAAGAGAGATGGCGCAACCAATGAGGCTG 540  
Db 4978 ACAAAATGCTGCCAACATCCCTCGACTTAAAGAGAGATGGCGCAACCAATGAGGCTG 5037  
Qy 541 GCATGAGGTCACTGACGGATTTATCGCAACTAGCAGTGGAGTTGGGAATGACAGATT 600  
Db 5038 GCATGAGGTCACTGACGGATTTATCGCAACTAGCAGTGGAGTTGGGAATGACAGATT 5097  
Qy 601 TGTATATGACCAATTTATATAAAGCTCAGGAATTTAGACTGCATCAAAATTTGACAGCA 660  
Db 5098 TGTATATGACCAATTTATATAAAGCTCAGGAATTTAGACTGCATCAAAATTTGACAGCA 5157  
Qy 661 AGTTGGTGAAGTCAACCTGTACCTAACCGAATTAAGTCAAGATTTGGGACCAAAAT 720  
Db 5158 AGTTGGTGAAGTCAACCTGTACCTAACCGAATTAAGTCAAGATTTGGGACCAAAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 780  
Db 5218 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGA 5277  
Qy 781 TATGATTAATCTTATGACTAAGTTAGGTGAGGAACAATCACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATCTTATGACTAAGTTAGGTGAGGAACAATCACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGTTTATACACCGGTAACCTATTCTATAGCTACAGCTCAACTCTTGGGAT 900  
Db 5338 TAGCGGTTTATACACCGGTAACCTATTCTATAGCTACAGCTCAACTCTTGGGAT 5397  
Qy 901 ACAGGTACTCTACCTTCAGTCGGGAACCTAAATATATGCGTCCACCTTATGGAAC 960  
Db 5398 ACAGGTACTCTACCTTCAGTCGGGAACCTAAATATATGCGTCCACCTTATGGAAC 5457  
Qy 961 CTATTCGGTAAGCAACAAGGGGATTTGCTCGGCACTTGTCCCAAAGTGGTGAACA 1020  
Db 5458 CTATTCGGTAAGCAACAAGGGGATTTGCTCGGCACTTGTCCCAAAGTGGTGAACA 5517  
Qy 1021 GGTCGGTTCTGTATAGAAAGACTTGACACTCATCTGTATAGAACTGACTTAAGATT 1080  
Db 5518 GGTCGGTTCTGTATAGAAAGACTTGACACTCATCTGTATAGAACTGACTTAAGATT 5577

Qy 1081 ATATTGTACAAAGATAGTAACGTTCCCTATGTCCTCCCTGGATTTATTTCTGCTTGAGCGG 1140  
Db 5578 ATATTGTACAAAGATAGTAACGTTCCCTATGTCCTCCCTGGATTTATTTCTGCTTGAGCGG 5637  
Qy 1141 CAATPAGGTGGGCTGTATGTACTCAAGACCGAAGGCGCACTTACTACACCATATGAC 1200  
Db 5638 CAATPAGGTGGGCTGTATGTACTCAAGACCGAAGGCGCACTTACTACACCATATGAC 5697  
Qy 1201 TATCAAGGTTCAATCGATCGCAACTGCAAGATGACAAACATGTAGTGTAAACCCGCC 1260  
Db 5698 TATCAAGGTTCAATCGATCGCAACTGCAAGATGACAAACATGTAGTGTAAACCCGCC 5757  
Qy 1261 GGGTATCATATCGCAAAACTATGAGAGCCGCTCTCTAATAGTATTAACAATCATGCCAA 1320  
Db 5758 GGGTATCATATCGCAAAACTATGAGAGCCGCTCTCTAATAGTATTAACAATCATGCCAA 5817  
Qy 1321 TGTATTATCTTATAGGCGGGATTAACCTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380  
Db 5818 TGTATTATCTTATAGGCGGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877  
Qy 1381 GAAGAAATATCTCAATCAAGATTCGCAAGTATTAACAGGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATCAAGATTCGCAAGTATTAACAGGCAATCTTGATATCTCAAC 5937  
Qy 1441 TGAAGTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATATAGTAAAGCA 1500  
Db 5938 TGAAGTTGGGAATGTCAACAATCGATCAGTAATGCTTTGAATATAGTAAAGCA 5997  
Qy 1501 CAGAAAATGACAAAGTCAATGTCAAACTGATAGACATCTGCTCATTAACCTATAT 1560  
Db 5998 CAGAAAATGACAAAGTCAATGTCAAACTGATAGACATCTGCTCATTAACCTATAT 6057  
Qy 1561 CGTTTGACTATCATATCTCTGTTTTTGGTATATTAAGCTGATTTAGACATGCTACCT 1620  
Db 6058 CGTTTGACTATCATATCTCTGTTTTTGGTATATTAAGCTGATTTAGACATGCTACCT 6117  
Qy 1621 AATGTACAGCAAAAGGCGCAACAACCTTATTTAGCTTGGGAATTAATCTTACA 1680  
Db 6118 AATGTACAGCAAAAGGCGCAACAACCTTATTTAGCTTGGGAATTAATCTTACA 6177  
Qy 1681 TCAAGTAGAGCCATCAACAAATATGGAACACAGATGAGGAAGGAAGTTCCCTAATAG 1740  
Db 6178 TCAAGTAGAGCCATCAACAAATATGGAACACAGATGAGGAAGGAAGTTCCCTAATAG 6237  
Qy 1741 TAAATTTGTGAAGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACTACCGGT 1800  
Db 6238 TAAATTTGTGAAGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACTACCGGT 6297  
Qy 1801 TGTATGATGACCAAGACGATATACGGGTGAAACGGTAAAGAGGCGCCCTCAATTGC 1860  
Db 6298 TGTATGATGACCAAGACGATATACGGGTGAAACGGTAAAGAGGCGCCCTCAATTGC 6357  
Qy 1861 GAGCGAGGCTTCAACACCTCGTTCTACCGCTTCAACGACAGTCTCAATCATGAGAC 1920  
Db 6358 GAGCGAGGCTTCAACACCTCGTTCTACCGCTTCAACGACAGTCTCAATCATGAGAC 6417  
Qy 1921 CGCGCGCTTACCAAGTTGCGTTAGAGAAATGATGAAGAGGCAAAAAATACATGCGC 1980  
Db 6418 CGCGCGCTTACCAAGTTGCGTTAGAGAAATGATGAAGAGGCAAAAAATACATGCGC 6477  
Qy 1981 TTGATATTCGGATTCGATCTTATTTTAAACAGTATGACTTTGGCTATATCTGATGCC 2040  
Db 6478 TTGATATTCGGATTCGATCTTATTTTAAACAGTATGACTTTGGCTATATCTGATGCC 6537  
Qy 2041 TCCCTTTATATAGCATGGGGCTAGACACCTTAGGCAATCTTGTATAGGCATACGACCTAGG 2100  
Db 6538 TCCCTTTATATAGCATGGGGCTAGACACCTTAGGCAATCTTGTATAGGCATACGACCTAGG 6597  
Qy 2101 ATTTCCAGGCGAGAGAAAGATTACATCTTACCTTGATTCATCAAGATGTAGAT 2160  
Db 6598 ATTTCCAGGCGAGAGAAAGATTACATCTTACCTTGATTCATCAAGATGTAGAT 6657  
Qy 2161 AGGATATATAGCAAGTGGCTTGATGCTCCGTTGGCATTTGTTAAATACTGAGACCA 2220

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Db 6658 AGATATATATAGCAAGTGGCCCTTGAGTCTCGTTGGCATTTGTAATAATCGAGCCCA 6717
Qy 2221 ATTATGAACGCAATTAACATCTCTCTTATGAGTTATGAGGCGCAACAGAGTGGG 2280
Db 6718 ATTATGAACGCAATTAACATCTCTCTTATGAGTTATGAGGCGCAACAGAGTGGG 6777
Qy 2281 TGGGGGGCACCTATCATGAGCCAGATTTATAGGGGGATAGGCMAAGAACTCATTTGA 2340
Db 6778 TGGGGGGCACTATCATGAGCCAGATTTATAGGGGGATAGGCMAAGAACTCATTTGA 6837
Qy 2341 GATGATGCTAGTATGTCACATCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 6838 GATGATGCTAGTATGTCACATCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 6897
Qy 2401 ATCCGGGGCGCTACTATACAGATCAGGTTGCACTGMAATCCCTCATTTGACATGAGTCT 2460
Db 6898 ATCCGGGGCGCTACTATACAGATCAGGTTGCACTGMAATCCCTCATTTGACATGAGTCT 6957
Qy 2461 ACCCATTAAGTCTACACCCATATATATATTTGTCTGGATCAGAGATCACTCATTTCA 2520
Db 6558 ACCCATTAAGTCTACACCCATATATATATTTGTCTGGATCAGAGATCACTCATTTCA 7017
Qy 2521 TATCAGTATTTAGCACTTGTGTGCTCGGACATCTGCAACAGGAGGGTATTTCTTTCT 2580
Db 7018 TATCAGTATTTAGCACTTGTGTGCTCGGACATCTGCAACAGGAGGGTATTTCTTTCT 7077
Qy 2581 ACTTGGGTTTCCATCAACCTGGAAGCAACCCMAATCGGAAGTCTTGAGATGTAGTGA 2640
Db 7078 ACTTGGGTTTCCATCAACCTGGAAGCAACCCMAATCGGAAGTCTTGAGATGTAGTGA 7137
Qy 2641 ACTCCCGTGGTGTGATATGATCTGTGCTGMAAGTCAAGAGACAGAGAGAAAGATTAT 2700
Db 7138 ACTCCCGTGGTGTGATATGATCTGTGCTGMAAGTCAAGAGACAGAGAGAAAGATTAT 7197
Qy 2701 AACTCAGCTGTCCCTACGCGGATGATCATGAGAGGTTAGGGTTTCAAGGCGCAATACCA 2760
Db 7198 AACTCAGCTGTCCCTACGCGGATGATCATGAGAGGTTAGGGTTTCAAGGCGCAATACCA 7257
Qy 2761 GAAAAGGACCTAGATGTCAACAATTTATCGGGGACTGGGGTGGCCACTACCCAGAGATA 2820
Db 7258 GAAAAGGACCTAGATGTCAACAATTTATCGGGGACTGGGGTGGCCACTACCCAGAGATA 7317
Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGGATGATGTTCTCAGTCTACGAGGGTTAAAAACC 2880
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGGATGATGTTCTCAGTCTACGAGGGTTAAAAACC 7377
Qy 2881 AATTCAACCAAGTGAACATGTAACAGAAAGGAATATGATATACAGCGATACATGAC 2940
Db 7378 AATTCAACCAAGTGAACATGTAACAGAAAGGAATATGATATACAGCGATACATGAC 7437
Qy 2941 ACATGCCCAAGTGAACAGATTAACAGATTTGGAATGCGCAAGTCTTCTATTAAGCTTGA 3000
Db 7438 ACATGCCCAAGTGAACAGATTAACAGATTTGGAATGCGCAAGTCTTCTATTAAGCTTGA 7497
Qy 3001 CGGTTTGGTGGAAAGCATACAGAGGCTATCTTATTAACAGAGTCAACATCTTA 3060
Db 7498 CGGTTTGGTGGAAAGCATACAGAGGCTATCTTATTAACAGAGTCAACATCTTA 7557
Qy 3061 GGGCAGAACCCGATAGTACTGTACCGGCCAACAAGTCAAGTCACTCATGAGGGGCGAAGGC 3120
Db 7558 GGGCAGAACCCGATAGTACTGTACCGGCCAACAAGTCAAGTCACTCATGAGGGGCGAAGGC 7617
Qy 3121 AGAATTTCTACAGTAGGACATCTCATTTCTTTGATACAGAGGGTCACTACTTCTCT 3180
Db 7618 AGAATTTCTACAGTAGGACATCTCATTTCTTTGATACAGAGGGTCACTACTTCTCT 7677
Qy 3181 CCGCGGTTATTAATCCATAGAGTCAAGTCAAGAAAGAGCACTCTTCAATGCTTAT 3240
Db 7678 CCGCGGTTATTAATCCATAGAGTCAAGTCAAGAAAGAGCACTCTTCAATGCTTAT 7737
Qy 3241 ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTACAGAAAGATGCCCC 3300
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Db 7738 ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTACAGAAAGATGCCCC 7797
Qy 3301 AACTGTGTGTACTGAGATCTATACAGATCCATATCCCTTAATCTTATAGAAACC 3358
Db 7798 AACTGTGTGTACTGAGATCTATACAGATCCATATCCCTTAATCTTATAGAAACC 7855

RESULT 5
ADM78414
ID ADM78414 standard; cDNA; 5292 BP.
XX
AC ADM78414;
XX
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #10.
XX
KW Newcastle disease virus; T7 RNA polymerase; Hep-2 cell; influenza virus;
KW infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
PN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
PA (SAMAL/) SAMAL S K.
PA (HUAN/) HUANG Z.
PI Samal SK, Huang Z;
XX
XX WPI; 2004-051891/05.
XX
DR Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L gene and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L gene, useful for producing vaccine
PT vector.
XX
PS Example 3; Page 12-14; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesizing T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesizing T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
CC cells, mammalian cells, avian cells or Hep-2 cells infected with a
CC vaccinia virus that can synthesize T7 RNA polymerase. The recombinant
CC virus is useful for vaccinating an avian animal against Newcastle disease
CC or an avian pathogen chosen from influenza virus, infectious bursal
CC disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
CC virus, Marek's disease virus, avian leukosis virus, avian adenovirus and
CC avian pneumovirus, where the avian animal is in need of the immunisation,
CC which involves administering the recombinant virus to the avian animal,
CC where the open reading frame of the foreign gene encodes an immunogenic
CC protein of the avian pathogen against which the avian animal is
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CC Immunized. The recombinant virus is also useful for immunising a mammal  
CC against a non-avian pathogen such as severe acute respiratory syndrome-  
CC causing virus (SARS virus), human respiratory syncytial virus, human  
CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.  
CC This sequence represents Newcastle disease virus recombinant cDNA of the  
CC invention.

XX Sequence 5292 BP; 1574 A; 1207 C; 1186 G; 1324 T; 0 U; 1 Other;

Query Match 96.5%; Score 3240.4; DB 12; Length 5292;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 3267; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

QY 82 TATGATGCTGATATCCGGGTGGCTGGCACTGAGTTGATCTGTCCGGCAACCTCAT 141  
DB 1 TATGATGCTGATATCCGGGTGGCTGGCTGATGATGATGATGATGATGATGATGAT 60  
QY 142 TGATGGCAGGCTTTTGCAAGCTGCAAGAAATTTGGTTACAGAGAACAAAGCCGTCAACAT 201  
DB 61 TGATGGCAGGCTTTTGCAAGCTGCAAGAAATTTGGTTACAGAGAACAAAGCCGTCAACAT 120  
QY 202 ATACACCTCATCCAGACAGGATCATATGATTAGTCTCTCCGAACTGCCCAAGGA 261  
DB 121 ATACACCTCATCCAGACAGGATCATATGATTAGTCTCTCTCCGAACTGCCCAAGGA 180  
QY 262 TAAAGAGCATGTGCGAAAGCCCTTGGATGATACAAACAGACATTGACACTTTGCT 321  
DB 181 TAAAGAGCATGTGCGAAAGCCCTTGGATGATACAAACAGACATTGACACTTTGCT 240  
QY 322 CACCCCTTGGTGAATCTTATCCGTAGATACAAAGATCTGTGATCTATCTTGGAGGGGG 381  
DB 241 CACCCCTTGGTGAATCTTATCCGTAGATACAAAGATCTGTGATCTATCTTGGAGGGGG 300  
QY 382 GAGACAGAGGCGCTTATAGCGCGCATTTATGGCGGTGGCTTTGGGGTTGCAATGTC 441  
DB 301 GAGACAGAGGCGCTTATAGCGCGCATTTATGGCGGTGGCTTTGGGGTTGCAATGTC 360  
QY 442 CGCACAATTAACAGCGCGCGAGCTGTGATACAAAGCCAAACAAATCTGCGCAATCTCT 501  
DB 361 CGCACAATTAACAGCGCGCGAGCTGTGATACAAAGCCAAACAAATCTGCGCAATCTCT 420  
QY 502 CCGAATTAAGAGAGCAATGCGCGCAACCAATGAGGCTGTGATGAGTCACTGACGAT 561  
DB 421 CCGAATTAAGAGAGCAATGCGCGCAACCAATGAGGCTGTGATGAGTCACTGACGAT 480  
QY 562 ATGCAACTGACAGTGGCAGTTGGGAAAGATGACAGATTTGTTATGACCAATTAATAA 621  
DB 481 ATGCAACTGACAGTGGCAGTTGGGAAAGATGACAGATTTGTTATGACCAATTAATAA 540  
QY 622 AACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCAAGTTGGTGTAGACTCAACT 681  
DB 541 AACAGCTCAGGAATTAAGCTGATCAAAATTTGACAGCAAGTTGGTGTAGACTCAACT 600  
QY 682 GTACCTTAACCGAATTTGATCAAGTATTCGACCAAAATCACTTCACTGCTTTAAACAA 741  
DB 601 GTACCTTAACCGAATTTGATCAAGTATTCGACCAAAATCACTTCACTGCTTTAAACAA 660  
QY 742 GGTGACATTCAGGCACTTTAACAATCTAGCTGTGGAAATATGGAATTAATTAATGACTAA 801  
DB 661 GGTGACATTCAGGCACTTTAACAATCTAGCTGTGGAAATATGGAATTAATTAATGACTAA 720  
QY 802 GTTAGGTGTAGGAAACAATCAATCACTCACTTAATCGGTAGCGCTTTAAACCGGTAA 861  
DB 721 GTTAGGTGTAGGAAACAATCACTCACTTAATCGGTAGCGCTTTAAACCGGTAA 780  
QY 862 CCGTATTTATAGACTCAAGACTCAACTCTTGGGTATACAGGTAACTCTTCACTTCACT 921  
DB 781 CCGTATTTATAGACTCAAGACTCAACTCTTGGGTATACAGGTAACTCTTCACTTCACT 840  
QY 922 CGGGAACCTAAATATATGCTGACCTACTTGGAAACCTTAACGTAAGCAACACAG 981  
DB 841 CGGGAACCTAAATATATGCTGACCTACTTGGAAACCTTAACGTAAGCAACACAG 900

QY 982 GGGATTTGCTCGGCACTGTGCTCCCAAAAGTGACACAGGTGCGTCTGTGATAGAAAGA 1041  
DB 901 GGGATTTGCTCGGCACTGTGCTCCCAAAAGTGACACAGGTGCGTCTGTGATAGAAAGA 960  
QY 1042 ACTTGACACCTCACTGATGATAGAACTGACTGATTTATTTATGTAACAAGATAGTAAC 1101  
DB 961 ACTTGACACCTCACTGATGATAGAACTGACTGATTTATTTATGTAACAAGATAGTAAC 1020  
QY 1102 GTTCCCTATGTCCCTGGTATTTATTTCTGTGAGCGGCAATAGTCCGCTGTATGTA 1161  
DB 1021 GTTCCCTATGTCCCTGGTATTTATTTCTGTGAGCGGCAATAGTCCGCTGTATGTA 1080  
QY 1162 CTCAAAACCGAAGCGCACTTACTACACCAATACATATCATCAAGATTCAGTCATCCG 1221  
DB 1081 CTCAAAACCGAAGCGCACTTACTACACCAATACATATCATCAAGATTCAGTCATCCG 1140  
QY 1222 CAATGCAAGATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1281  
DB 1141 CAATGCAAGATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
QY 1282 TGGAGAAAGCGGTGCTCTAAATAGATTAACATCATGCAATGTTTATCTTAAAGCGGAT 1341  
DB 1201 TGGAGAAAGCGGTGCTCTAAATAGATTAACATCATGCAATGTTTATCTTAAAGCGGAT 1260  
QY 1342 AACTTTAAGGCTCAGTGGGGAATTCAGATGATCTTATCAGAAAGATTCATACAAAGA 1401  
DB 1261 AACTTTAAGGCTCAGTGGGGAATTCAGATGATCTTATCAGAAAGATTCATACAAAGA 1320  
QY 1402 TTCTCAAGTAAATATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGTCAACA 1461  
DB 1321 TTCTCAAGTAAATATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGTCAACA 1380  
QY 1462 CTCGATCAGTAATGCTTTGATTAAGTTAGAGAAAGCAAGAAACTAGACAAAGTCAA 1521  
DB 1381 CTCGATCAGTAATGCTTTGATTAAGTTAGAGAAAGCAAGAAACTAGACAAAGTCAA 1440  
QY 1522 TGTCAAACTGACTGACATCTGCTCATTAATCTATATGTTTGTGATCATATCTCT 1581  
DB 1441 TGTCAAACTGACTGACATCTGCTCATTAATCTATATGTTTGTGATCATATCTCT 1500  
QY 1582 TGTTTTGGTAACTTACCGCTGATTTAGCATGCTACCTAATGTAACAAGCAAAAGGCGCA 1641  
DB 1501 TGTTTTGGTAACTTACCGCTGATTTAGCATGCTACCTAATGTAACAAGCAAAAGGCGCA 1560  
QY 1642 ACAAACCTTATTTATGCTTGGGAAATTAATCTTATGATCAGATGAGAGCACTACAAA 1701  
DB 1561 ACAAACCTTATTTATGCTTGGGAAATTAATCTTATGATCAGATGAGAGCACTACAAA 1620  
QY 1702 AATGTGAACACAGATGAGAACGAGGTTTCCCTAATATGTAATTTGTGTAAAGTTCTGG 1761  
DB 1621 AATGTGAACACAGATGAGAACGAGGTTTCCCTAATATGTAATTTGTGTAAAGTTCTGG 1680  
QY 1762 TAGTCTGCTCAGTCAAGAGTAAAGAAACATCAACGCTGTGTGATGACCAAGGAGAT 1821  
DB 1681 TAGTCTGCTCAGTCAAGAGTAAAGAAACATCAACGCTGTGTGATGACCAAGGAGAT 1740  
QY 1822 ATACGGGTAGAAAGGTAAAGAGGCGCGCTCAATTCGAGAGCGGCTTCAACAACCTCC 1881  
DB 1741 ATACGGGTAGAAAGGTAAAGAGGCGCGCTCAATTCGAGAGCGGCTTCAACAACCTCC 1800  
QY 1882 GTTCTACCGCTTCAACGACCAACAGTCTCAATCATGACCGCGCTTACGCAAGTTGCG 1941  
DB 1801 GTTCTACCGCTTCAACGACCAACAGTCTCAATCATGACCGCGCTTACGCAAGTTGCG 1860  
QY 1942 TTAGAGAAATATGAAAGAGGCAAAATATCATGCGGCTGTGATTCGGGATTCGCAATC 2001  
DB 1861 TTAGAGAAATATGAAAGAGGCAAAATATCATGCGGCTGTGATTCGGGATTCGCAATC 1920  
QY 2002 TTATTTCTTAACAGTAGGACTTGGCTATATCTGTAGCTTCCCTTTTATATAGCATGGGG 2061  
DB 1921 TTATTTCTTAACAGTAGGACTTGGCTATATCTGTAGCTTCCCTTTTATATAGCATGGGG 1980  
QY 2062 GCTAGCACACCTTAGCGATCTTGTAGGCAATCCGACTAGGATTTTCCAGGGCAGAAAG 2121





CC useful for preparing a probe for extracting similar genes from a gene  
CC library or for identifying the presence of NDV virions in a sample obd.  
CC from poultry'. (Updated on 25-MAR-2003 to correct PA field.) (Updated on  
CC 27-AUG-2003 to correct OS field.)

XX Sequence 3825 BP; 1122 A; 898 C; 856 G; 949 T; 0 U; 0 Other;

Query Match 95.2%; Score 3196.4; DB 1; Length 3825;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 ACGGGTGAAGATCTGGATCCGGTTGGCGCCCTCCAGGNGCAAGATGGCTCCAGACC 60  
DB 1 ACGGGTGAAGATCTGGATCCGGTTGGCGCCCTCTAGGTGCAAGATGGGCCCCAGACC 60  
QY TTTCACCAAGAACCCAGACCTTATGATGCTACTATCCGGGTTGCGCTGACCTAGTTG 120  
DB TTTCACCAAGAACCCAGACCTTATGATGCTACTATCCGGGTTGCGCTGACCTAGTTG 120  
QY 121 CATCTGTCGGCAAACTTCATTTGATGGCAGGCTCTTGGACCTGCAAGAAATTGTGTAC 180  
DB 121 CATCTGTCGGCAAACTTCATTTGATGGCAGGCTCTTGGACCTGCAAGAAATTGTGTAC 180  
QY 181 AGGAGCAAAAGCCCTCAACATATACCTCATCCCAAGCAGATCAATCATAGTTAAGCT 240  
DB 181 AGGAGCAAAAGCCCTCAACATATACCTCATCCCAAGCAGATCAATCATAGTTAAGCT 240  
QY 241 CCTCCCAATCTGCGCAAGATAGAGAGCATGTGCGAAACCCCTTGGATGACATCA 300  
DB 241 CCTCCCAATCTGCGCAAGATAGAGAGCATGTGCGAAACCCCTTGGATGACATCA 300  
QY 301 CAGGACATTGACCACTTTGCTCACCCCTTGTGTACTCTATCCGTAGATACAAAGATC 360  
DB 301 CAGGACATTGACCACTTTGCTCACCCCTTGTGTACTCTATCCGTAGATACAAAGATC 360  
QY 361 TGTGACTACATCTGGAAGGGGGGAGACAGGGGGCTTATAGGCCCATTTATGGCGGT 420  
DB 361 TGTGACTACATCTGGAAGGGGGGAGACAGGGGGCTTATAGGCCCATTTATGGCGGT 420  
QY 421 GGCTCTTGGGGTTGCAACCTGCGCAAAATACAGCGGCGCAGCTCTGATACAAAGCAA 480  
DB 421 GGCTCTTGGGGTTGCAACCTGCGCAAAATACAGCGGCGCAGCTCTGATACAAAGCAA 480  
QY 481 ACAAAATGCTGCCAACAATCTCTCGCACTTAAAGAGAGCATTCGCGCAACCAATGAAGCT 540  
DB 481 ACAAAATGCTGCCAACAATCTCTCGCACTTAAAGAGAGCATTCGCGCAACCAATGAAGCT 540  
QY 541 GCATGAGCTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGCTT 600  
DB 541 GCATGAGCTCACTGACGGATTATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGCTT 600  
QY 601 TGTTAATGACCAATTTTATATAAAACAGCTCAGAGATTAAGCTGCAAAAATTGACAGCA 660  
DB 601 TGTTAATGACCAATTTTATATAAAACAGCTCAGAGATTAAGCTGCAAAAATTGACAGCA 660  
QY 661 AGTTGTGTGAGAGCTCAACCTGTACCTAACCGAAATTGACTACAGTATTCGGACCAAAAT 720  
DB 661 AGTTGTGTGAGAGCTCAACCTGTGTACCTAACCGAAATTGACTACAGTATTCGGACCAAAAT 720  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAAGGCACTTTAACATCTAGCTGTGGGAA 780  
DB 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAAGGCACTTTAACATCTAGCTGTGGGAA 780  
QY 781 TATGATTAATCTTATGACTAAGTTAGGTGAGGAAACATCACTCAGCTATTATTCGG 840  
DB 781 TATGATTAATCTTATGACTAAGTTAGGTGAGGAAACATCACTCAGCTATTATTCGG 840  
QY 841 TAGCGGCTTATCAACCGGTAAACCTTATCTATACGACTCAAGACTCAACTCTTGGGTAT 900  
DB 841 TAGCGGCTTATCAACCGGTAAACCTTATCTTGTAGCTCAAGACTCAACTCTTGGGTAT 900  
QY 901 ACAGGTAACTTACCTTACGTCGGGAACTTAATTAATGCGTGCACCTTCTTGGAAAC 960  
DB 901 ACAGGTAACTTACCTTACGTCGGGAACTTAATTAATGCGTGCACCTTCTTGGAAAC 960

DB 901 ACAGGTAACTTACCTTACGTCGGGAACTTAATTAATGCGTGCACCTTCTTGGAAAC 960  
QY 961 CTATTCGGTAAGCAACAACGAGGGATTTGCTCGGCACTTGTCACCAAAAGTGAGACA 1020  
DB 961 CTATTCGGTAAGCAACAACGAGGGATTTGCTCGGCACTTGTCACCAAAAGTGAGACA 1020  
QY 1021 GGTGGTTCTGTGATAGAAACCTTGAACCTCTGATCTGTATAGAACTGACTAGATT 1080  
DB 1021 GGTGGTTCTGTGATAGAAACCTTGAACCTCTGATCTGTATAGAACTGACTAGATT 1080  
QY 1081 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCCTGTATTTATTTCTGCTTGAACGG 1140  
DB 1081 ATATTGTACAAGAAATAGTAAGTTCCCTATGTCCCTGTATTTATTTCTGCTTGAACGG 1140  
QY 1141 CAATACATCGGCTGTATGTACTCAAAAGCCGAAAGGCGCACTTATCAACCATATCATGAC 1200  
DB 1141 CAATACATCGGCTGTATGTACTCAAAAGCCGAAAGGCGCACTATCGCATCATGAC 1200  
QY 1201 TATCAAAAGTTCACTATTCGCAACCTGCAAGATGACAAACATGTATGTATTAACCCGCC 1260  
DB 1201 TATCAAAAGTTCACTATTCGCAACCTGCAAGATGACAAACATGTATGTATTAACCCGCC 1260  
QY 1261 GGGTATCATATCGCAAACTATGGAAGAGCGGTCTCTAATAGATTAACATCATGAC 1320  
DB 1261 GGGTATCATATCGCAAACTATGGAAGAGCGGTCTCTAATAGATTAACATCATGAC 1320  
QY 1321 TGTTTATCTTACGCGGATTAACCTTTTACGCTCAGTGGGAAATTCAGTAACTTATCA 1380  
DB 1321 TGTTTATCTTACGCGGATTAACCTTTTACGCTCAGTGGGAAATTCAGTAACTTATCA 1380  
QY 1381 GAAGAAATCTCAATACAAAGTTCTCAAGTATTAATTAACAGGCAATTTGATATCTAC 1440  
DB 1381 GAAGAAATCTCAATACAAAGTTCTCAAGTATTAATTAACAGGCAATTTGATATCTAC 1440  
QY 1441 TGAAGTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTAAAGGAAACAA 1500  
DB 1441 TGAAGTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATTAAGTAAAGGAAACAA 1500  
QY 1501 CAGAAACCTAGCAAAAGTCAATGTCAAATGACTAGACATCTGCTCTCATTTACTATAT 1560  
DB 1501 CAGAAACCTAGCAAAAGTCAATGTCAAATGACTAGACATCTGCTCTCATTTACTATAT 1560  
QY 1561 CGTTTGACTATCATATCTCTGTTTGGTATTAAGCTGATTTCTAGATGCTACTCT 1620  
DB 1561 CGTTTGACTATCATATCTCTGTTTGGTATTAAGCTGATTTCTAGATGCTACTCT 1620  
QY 1621 AATGTACAAGCAAAAGGCGCAACAAAACCTTATTAAGCTTGGGAAATTAATCTAGA 1680  
DB 1621 AATGTACAAGCAAAAGGCGCAACAAAACCTTATTAAGCTTGGGAAATTAATCTAGA 1680  
QY 1681 TCAGATGAGCACTTACAAAATGTGAAACACAGATGAGGACGAAGGTTCCCTAATAG 1740  
DB 1681 TCAGATGAGCACTTACAAAATGTGAAACACAGATGAGGACGAAGGTTCCCTAATAG 1740  
QY 1741 TAATTTGTGAAAGTTCTGTGATGCTGTCAAGTTCAAGAGTTTAAGAAAAATCAACGGGT 1800  
DB 1741 TAATTTGTGAAAGTTCTGTGATGCTGTCAAGTTCTGAGAGTTTAAGAAAAATCAACGGGT 1800  
QY 1801 TGTAGATGACCAAAAGAGCATATACGGGTTAGAACGTTAAGAGAGGCGCCCTCAATTCG 1860  
DB 1801 TGTAGATGACCAAAAGAGCATATACGGGTTAGAACGTTAAGAGAGGCGCCCTCAATTCG 1860  
QY 1861 GAGCGAGGCTTCAACACTCGTTTCAACGCTTCAACGCAACAGTCTCAATCATATGAC 1920  
DB 1861 GAGCGAGGCTTCAACACTCGTTTCAACGCTTCAACGCAACAGTCTCAATCATATGAC 1920  
QY 1921 CGCGCGTTAGCAAGTTGCGTTAGAGATGATGAAAAGAGCAAAAAATCAATGCGCG 1980  
DB 1921 CGCGCGTTAGCAAGTTGCGTTAGAGATGATGAAAAGAGCAAAAAATCAATGCGCG 1980  
QY 1981 TTGATATTCGGGATGGAATCTTATCTTAAACGTATGTGACCTTGGCTATATCTGTAGCC 2040  
DB 1981 TTGATATTCGGGATGGAATCTTATCTTAAACGTATGTGACCTTGGCTATATCTGTAGCC 2040

QY 2041 TCCCTTTATATAGCATGGGGGCTAGCACAACCTAGCGATCTTGTAGGCATACCGATAGG 2100  
 DB 2041 TCCCTTTATATAGCATGGGGGCTAGCACAACCTAGCGATCTTGTAGGCATACCGATAGG 2100  
 QY 2101 ATTTCCAGGGCAGAAAGAAAGATTATCATCTTACACTTGGTTCATCAAGATGTAGTAT 2160  
 DB 2101 ATTTCTAGGGCAGAAAGAAAGATTATCATCTTACACTTGGTTCATCAAGATGTAGTAT 2160  
 QY 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGGTTGGCATTTGTAATTAAGTGAACACA 2220  
 DB 2161 AGGATATATAGCAAGTGGCCCTTGAAGTCTCGGTTGGCATTTGTAATTAAGTGAACACA 2220  
 QY 2221 ATATGAAACGCAATTAACATCTCTCTTATGAGTTAATGAGCTGCAACAAAGTGGG 2280  
 DB 2221 ATATGAAACGCAATTAACATCTCTCTTATGAGTTAATGAGCTGCAACAAAGTGGG 2280  
 QY 2281 TGGGGGCACTTATCATGACCCAGATTATATAGGGGGATAGCAAAAGAACTCATTTGA 2340  
 DB 2281 TGGGGGCACTTATCATGACCCAGATTATATAGGGGGATAGCAAAAGAACTCATTTGA 2340  
 QY 2341 GATGATGCTAGTATGTCATCATCTTATCCCTGTGATTTCAAGAACATCTGAATTTT 2400  
 DB 2341 GATGATGCTAGTATGTCATCATCTTATCCCTGTGATTTCAAGAACATCTGAATTTT 2400  
 QY 2401 ATCCCGGCGCTTACTACAGATCAGTTGCACTCGAATTAACCTCATTTGATGAGTGTCT 2460  
 DB 2401 ATCCCGGCGCTTACTACAGATCAGTTGCACTCGAATTAACCTCATTTGATGAGTGTCT 2460  
 QY 2461 ACCCATTAAGTCTACACCCATTAATGTAAATTTGTCTGAGTACAGAGATCACTCATTTCA 2520  
 DB 2461 ACCCATTAAGTCTACACCCATTAATGTAAATTTGTCTGAGTACAGAGATCACTCATTTCA 2520  
 QY 2521 TATATGATTTAGACATTTGGTGTCTCCGACATCTGCAACAGAGAGGTATTTCTTTCT 2580  
 DB 2521 TATATGATTTAGACATTTGGTGTCTCCGACATCTGCAACAGAGAGGTATTTCTTTCT 2580  
 QY 2581 ACTCTGGGTTTCATCAACCTGAGCAGACCCAAATCGGAAGTCTTGTGAGTGTAGTGTCA 2640  
 DB 2581 ACTCTGGGTTTCATCAACCTGAGCAGACCCAAATCGGAAGTCTTGTGAGTGTAGTGTCA 2640  
 QY 2641 ACTCCCTTGAAGTGTGATATGCTGTGCTCGAAGTCAAGAGACAGAGAAAGATTTAT 2700  
 DB 2641 ACTCCCTTGAAGTGTGATATGCTGTGCTCGAAGTCAAGAGACAGAGAAAGATTTAT 2700  
 QY 2701 AACTCAGTGTCTTCCATCGCGGATGTATAGTGGAGTTAGAGTTGACAGGCGCATGACAC 2760  
 DB 2701 AACTCAGTGTCTTCCATCGCGGATGTATAGTGGAGTTAGAGTTGACAGGCGCATGACAC 2760  
 QY 2761 GAAAAGGACCTAGATGTCAACAATTATTCGGGGGCTGGGTGGCAACTACCCAGAGATA 2820  
 DB 2761 GAAAAGGACCTAGATGTCAACAATTATTCGGGGGCTGGGTGGCAACTACCCAGAGATA 2820  
 QY 2821 GGGGGTGGATCTTTTATTTGACAGCGCGCTATGTCTTCACTACGAGGGTTAAACC 2880  
 DB 2821 GGGGGTGGATCTTTTATTTGACAGCGCGCTATGTCTTCACTACGAGGGTTAAACC 2880  
 QY 2881 AATTACCCAGTGAACCTGTACAGAGAGGAAATGTGATATACAGCGATACATGAC 2940  
 DB 2881 AATTACCCAGTGAACCTGTGTACAGAGAGGAAATGTGATATACAGCGATACATGAC 2940  
 QY 2941 ACATGCCCAAGTGAAGCAAGATCAACCAATTGGAATGGCAAGTCTTCTATTAAGCTTGA 3000  
 DB 2941 ACATGCCCAAGTGAAGCAAGATCAACCAATTGGAATGGCAAGTCTTCTATTAAGCTTGA 3000  
 QY 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060  
 DB 3001 CGGTTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGTGTCAACATCTTTA 3060  
 QY 3061 GGGGAAAGCCGGTACTGACTGTACCGGCCAACACAGTCAACCTATGAGGGGCGAGAGGC 3120  
 DB 3061 GGGGAAAGCCGGTACTGACTGTACCGGCCAACACAGTCAACCTATGAGGGGCGAGAGGC 3120

QY 3121 AGAATTCTCACAGTAGGAGCATCTCATTTTCTTGTATATACAGAGGTCATCATCTTCT 3180  
 DB 3121 AGAATTCTCACAGTAGGAGCATCTCATTTTCTTGTATATACAGAGGTCATCATCTTCT 3180  
 QY 3181 CCCGGTTATATATCCATAGAGTACAGCAACAAACAGCAGCTTCTATAGTCCCTAT 3240  
 DB 3181 CCCGGTTATATATCCATAGAGTACAGCAACAAACAGCAGCTTCTATAGTCCCTAT 3240  
 QY 3241 ACATTCAATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGAGCTTACAGAAATGCC 3300  
 DB 3241 ACATTCAATGCTTCACTCGGCGCAGTAGTATCCCTTCCAGAGCTTACAGAAATGCC 3300  
 QY 3301 AACTCGTGTGTACTGAGAGTCTATACAGATCATATCCCTTAATCTTATAGAAAC 3358  
 DB 3301 AACTCGTGTGTACTGAGAGTCTATACAGATCATATCCCTTAATCTTATAGAAAC 3358

RESULT 7  
 ADM78418  
 ID ADM78418 standard; cDNA; 5291 BP.  
 XX  
 AC ADM78418;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Newcastle disease virus recombinant cDNA #14.  
 XX  
 KW Newcastle disease virus; T7 RNA polymerase; HEP-2 cell; influenza virus; infectious bursal disease virus; rotavirus; infectious bronchitis virus; chicken anaemia virus; Marek's disease virus; avian leukosis virus; avian adenovirus; avian pneumovirus;  
 KW severe acute respiratory syndrome-causing virus; SARS;  
 KW human respiratory syncytial virus; human immunodeficiency virus; hepatitis virus; measles virus; mumps virus; antiviral; ss.  
 KW  
 OS Newcastle disease virus.  
 XX  
 PN US2003224017-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 XX 19-MAY-2003; 2003US-00440419.  
 XX  
 PF 05-MAY-2000; 2000WO-US006700.  
 XX  
 PR 06-MAR-2002; 2002US-00926431.  
 PR 17-MAY-2002; 2002US-0381462P.  
 XX  
 PA (SAMA/) SAMAL S K.  
 PA (HUN/) HUANG Z.  
 XX  
 PI Samal SK, Huang Z;  
 XX  
 DR WPI: 2004-051891/05.  
 XX  
 PT Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN, L genes and foreign nucleotide complex inserted before NP gene, between P, M genes and/or between HN, L genes, useful for producing vaccine vector.  
 PT  
 PT  
 PT  
 XX  
 XX  
 XX  
 XX  
 XX Example 3; Page 18-19; 41pp; English.  
 XX  
 CC The invention relates to an antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign nucleotide complexes inserted between genes. The invention also relates to cDNA related to the RNA, a plasmid comprising the cDNA, a cell comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a recombinant Newcastle disease virus comprising the RNA. The RNA is useful for producing a recombinant Newcastle disease virus by providing cells capable of synthesizing T7 RNA polymerase, transfecting the cells with a plasmid comprising cDNA or a protein of interest to obtain transfected cells in a medium and isolating Newcastle disease virus from a supernatant of the medium, where the cells capable synthesizing T7 RNA polymerase are from a cell line expressing T7 RNA polymerase or plant

CC cells, mammalian cells, avian cells or HEP-2 cells infected with a  
 CC vaccinia virus that can synthesize T7 RNA polymerase. The recombinant  
 CC virus is useful for vaccinating an avian animal against Newcastle disease  
 CC or an avian pathogen chosen from influenza virus, infectious bursal  
 CC disease virus, rotavirus, infectious bronchitis virus, chicken anemia  
 CC virus, Marek's disease virus, avian leukosis virus, avian adenovirus and  
 CC avian pneumovirus, where the avian animal is in need of the immunisation,  
 CC which involves administering the recombinant virus to the avian animal,  
 CC where the open reading frame of the foreign gene encodes an immunogenic  
 CC protein of the avian pathogen against which the avian animal is  
 CC immunized. The recombinant virus is also useful for immunising a mammal  
 CC against a non-avian pathogen such as severe acute respiratory syndrome-  
 CC causing virus (SARS virus), human respiratory syncytial virus, human  
 CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.  
 CC This sequence represents Newcastle disease virus recombinant cDNA of the  
 CC invention.

XX Sequence 5291 BP; 1565 A; 1202 C; 1186 G; 1332 T; 0 U; 6 Other;

Query Match 72.7%; Score 2441.6; DB 12; Length 5291;  
 Best Local Similarity 97.0%; Pred. No. 0;  
 Matches 2486; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 796 GACTAATTGGTGTAGGAAACATCACTCAGCTCAATTATCGGTAGCGGCTTAATCAC 855  
 Db 1 GACTAATTGGTGTAGGAAACATCACTCAGCTCAATTATCGGTAGCGGCTTAATCAC 60  
 Qy 856 CGGTAAACCTTATTTATACGACTCAGAGACTCACTCTTGGGTATACAGTAACTTACC 915  
 Db 61 CGGCAACCTTATTTCTGACACTCAGAGACTCACTCTTGGGTATACAGTAACTTACC 120  
 Qy 916 TTCACTCGGAAACCTAATAATATATGCGTCCACTTCTGAAACCTTATCCGTAAGCAC 975  
 Db 121 TTCACTCGGAAACCTAATAATATATGCGTCCACTTCTGAAACCTTATCCGTAAGCAC 180  
 Qy 976 ACCCAGGGATTTGGCTCGGACTGTGCCAAAGGTGTACAGAGTGGTCTGTGAT 1035  
 Db 181 ACCCAGGGATTTGGCTCGGACTGTGCCAAAGGTGTACAGAGTGGTCTGTGAT 240  
 Qy 1036 AGAAGAATTGACACCTCATCTGTATAGAAAGTACTAGATTATTTATGTACAAAGAT 1095  
 Db 241 AGAAGAATTGACACCTCATCTGTATAGAAAGTACTAGATTATTTATGTACAAAGAT 300  
 Qy 1096 AGTAACCTTCCCTATGTCCTCCGTGATTTATCTCTGTTGAGGGCAATACGTGGCTTG 1155  
 Db 301 AGTAACCTTCCCTATGTCCTCCGTGATTTATCTCTGTTGAGGGCAATACGTGGCTTG 360  
 Qy 1156 TATGTACTCAAAAGCCGAAGCGGACTTACTACACCTATGATCTATCAAAAGTTGAGT 1215  
 Db 361 TATGTACTCAAAAGCCGAAGCGGACTTACTACACCTATGATCTATCAAAAGTTGAGT 420  
 Qy 1216 CATCGCAACTGCAAGATGACCAATGATGATGTGTAAACCCCGGGGTATCATATGCA 1275  
 Db 421 CATCGCAACTGCAAGATGACCAATGATGATGTGTAAACCCCGGGGTATCATATGCA 480  
 Qy 1276 AAATCTAGAGAAAGCCGTGTCTCTAATAGATTAACAATCATGCAATGTTTATCTTAGG 1335  
 Db 481 AAATCTAGAGAAAGCCGTGTCTCTAATAGATTAACAATCATGCAATGTTTATCTTAGG 540  
 Qy 1336 CGGGATTAATTAAAGGCTCAGTGGGGAAATTCAGATTAATTATCAAGAAATATCTCAAT 1395  
 Db 541 CGGGATTAATTAAAGGCTCAGTGGGGAAATTCAGATTAATTATCAAGAAATATCTCAAT 600  
 Qy 1396 ACAAGATTTCAAGTAAATTAATTAACAGGCAATCTGATATCTCAACTGAGCTTGGAAATGT 1455  
 Db 601 ACAAGATTTCAAGTAAATTAATTAACAGGCAATCTGATATCTCAACTGAGCTTGGAAATGT 660  
 Qy 1456 CAACAATCTGATCAGTAAATGTTGAATTAAGTAAAGAGAAAGCAAGAAACTAGACAA 1515  
 Db 661 CAACAATCTGATCAGTAAATGTTGAATTAAGTAAAGAGAAAGCAAGAAACTAGACAA 720  
 Qy 1516 AGTCATGTCAAACTAGACATCTGCTCTATTAACCTATATCGTTTGAATATCAT 1575

Db 721 AGTCATGTCAAACTAGACATCTGCTCTATTAACCTATATCGTTTGAATATCAT 780  
 Qy 1576 ATCTCTGTTTTGGTATTAAGTACTGATTTCTAGCATGCTACTTAATGTACAAAGCAAA 1635  
 Db 781 ATCTCTGTTTTGGTATTAAGTACTGATTTCTAGCATGCTACTTAATGTACAAAGCAAA 840  
 Qy 1636 GGGCCAAACAAAACCTTATTAAGGCTTGGGAATTAATCTAGATGATGAGAGCAC 1695  
 Db 841 GGGCCAAACAAAACCTTATTAAGGCTTGGGAATTAATCTAGATGATGAGAGCAC 900  
 Qy 1696 TACAAAATGTGAACAGATGAGAAAGCAAGGTTTCCCTAATATGATTAATTTGTGTGAAG 1755  
 Db 901 TACAAAATGTGAACAGATGAGAAAGCAAGATATCCCAATATGATTAATTTGTGTGAAG 960  
 Qy 1756 TTCTGTAGTCTGTCAAGTCAAGAGTTAAAGAAAACTACCGGTTAGATGACCAAG 1815  
 Db 961 TTCTGTAGTCTGTCAAGTCAAGAGTTAAAGAAAACTACCGGTTAGATGACCAAG 1020  
 Qy 1816 GAGCATTAAGGGTAAAGACGTAAAGAGAGCCGCCCTCAATTGCGAGCCAGGCTTACA 1875  
 Db 1021 GAGCATTAAGGGTAAAGACGTAAAGAGAGCCGCCCTCAATTGCGAGCCAGGCTTACA 1080  
 Qy 1876 ACCTCGGTCTACCGCTTCAACCGACCAAGTCCCTCAATCAATGACCGCGCTTAAGCCAA 1935  
 Db 1081 ACCTCGGTCTACCGCTTCAACCGACCAAGTCCCTCAATCAATGACCGCGCTTAAGCCAA 1140  
 Qy 1936 GTTCCGTTAGAGATGATGAAAGAGAGCAAAAAATACATGCGGCTTGATATTCGGGATT 1995  
 Db 1141 GTTCCGTTAGAGATGATGAAAGAGAGCAAAAAATACATGCGGCTTGATATTCGGGATT 1200  
 Qy 1996 GCAATCTTAATTTTAAGATGATGACCTTGCTATATCTGATGCTCCCTTTATATAGC 2055  
 Db 1201 GCAATCTTAATTTTAAGATGATGACCTTGCTATATCTGATGCTCCCTTTATATAGC 1260  
 Qy 2056 ATGGGGGCTACACACCTTAACGATCTTTGATAGCAATCCGATAGATTTCAAGGGCAAA 2115  
 Db 1261 ATGGGGGCTACACACCTTAACGATCTTTGATAGCAATCCGATAGATTTCAAGGGCAAA 1320  
 Qy 2116 GAAAGATTAATCATCTACCTGTTCCATCAAGATGATGATGATGATGATTAATACCA 2175  
 Db 1321 GAAAGATTAATCATCTGCTGATTTGATTAATGAGATGATGATGATGATTAATACCA 1380  
 Qy 2176 GTGGCCCTTAAGTCTCCGTGGGCAATTTTAATCTGAGACCAATTAATGAAGGCAATA 2235  
 Db 1381 GTGGCCCTTAAGTCTCCGTGGGCAATTTTAATCTGAGACCAATTAATGAAGGCAATA 1440  
 Qy 2236 ACATCTCTCTTATGATGATTAATGAGCTGCAACCAAGTGGGTGGGGGCACTATC 2295  
 Db 1441 ACATCTCTCTTATGATGATTAATGAGCTGCAACCAAGTGGGTGGGGGCACTATC 1500  
 Qy 2296 CATGACCAAGATTAATTAAGGGGGGATAGGCAAAAGACTCATTTGATGATGATGAT 2355  
 Db 1501 CATGACCAAGATTAATTAAGGGGGGATAGGCAAAAGACTCATTTGATGATGATGATGAT 1560  
 Qy 2356 GTCAATCATTTCTATCCCTCTGCAATTTCAAGAAACATGTAATTTATCCGGGCGCTTACT 2415  
 Db 1561 GTCAATCATTTCTATCCCTCTGCAATTTCAAGAAACATGTAATTTATCCGGGCGCTTACT 1620  
 Qy 2416 ACGAGATCAGTTGCACTGCAATACCTCATTTTGAACATGAGTGCTACCACTTACTGCTAC 2475  
 Db 1621 ACGAGATCAGTTGCACTGCAATACCTCATTTTGAACATGAGTGCTACCACTTACTGCTAC 1680  
 Qy 2476 ACCCATTAATTAATTAATTTGCTGATGACAGATCACTCATTTATTAATGATTAATTA 2535  
 Db 1681 ACCCATTAATTAATTAATTTGCTGATGACAGATCACTCATTTATTAATGATTAATTA 1740  
 Qy 2536 CTGTTGTGCTCCGAGACATTTGCAACAGGAGGATTTCTTTTCTACTCTGCGTTCCATC 2595  
 Db 1741 CTGTTGTGCTCCGAGACATTTGCAACAGGAGGATTTCTTTTCTACTCTGCGTTCCATC 1800  
 Qy 2596 AACCTGAGACACCCCAAAATCGGAAGTCTTGGAGTGTGATGATCACTCCCTGAGGTTGT 2655  
 Db 1801 AACCTGAGACACCCCAAAATCGGAAGTCTTGGAGTGTGATGATCACTCCCTGAGGTTGT 1860

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QY 2656 GATATGCTGTGCTGAAAGTCAAGAGAGAGAGAAATTAATCACTGCTGCTT 2715
XX |||
XX 1861 GATATGCTGTGCTGAAAGTCAAGAGAGAGAGAAATTAATCACTGCTGCTT 1920
XX |||
QY 2716 ACGGGATGATGATGAGAGGTTAGGCTTCAAGGCGCCAGTACCAAGAAAGAGCTTAAT 2775
XX |||
XX 1921 ACGGTGATGAGATGAGAGGTTAGGCTTCAAGGCGCCAGTACCAAGAAAGAGCTTAAC 1980
XX |||
QY 2776 GTCAACAATTAATTCGGGAGCTGGGTGGCAACTACCAAGAGATAGGGGGTGGATCTTTT 2835
XX |||
XX 1981 GTCAACAATTAATTCGGGAGCTGGGTGGCAACTACCAAGAGATAGGGGGTGGATCTTTT 2040
XX |||
QY 2836 ATTGACAGCCGCGATGATGCTGAGTCAAGAGAGGTTAAACCAATTCACCAAGTAC 2895
XX |||
XX 2041 ATTGACAGCCGCGATGATGCTGAGTCAAGAGAGGTTAAACCAATTCACCAAGTAC 2100
XX |||
QY 2896 ACTGTACAGGAAGGAATATGATGATATCAAGGATACATGACATGCCAGATGAG 2955
XX |||
XX 2101 ACTGTACAGGAAGGAATATGATGATATCAAGGATACATGACATGCCAGATGAG 2160
XX |||
QY 2956 CAAGACTACCGAGATTCGAATGGCCAAAGTCTTGATTAAGCTTGACGGTTTGGGGAAA 3015
XX |||
XX 2161 CAAGACTACCGAGATTCGAATGGCCAAAGTCTTGATTAAGCTTGACGGTTTGGGGAAA 2220
XX |||
QY 3016 CGCATACAGCAGGCTATCTTATCTATCAAGGTTCAACATCTTAAAGCGAAACCCGGTA 3075
XX |||
XX 2221 CGCATACAGCAGGCTATCTTATCTATCAAGGTTCAACATCTTAAAGCGAAACCCGGTA 2280
XX |||
QY 3076 CTGACTGTACCGCCCAACACAGTCACTCATGAGGGGCCGAAGGCAATTCACAGTA 3135
XX |||
XX 2281 CTGACTGTACCGCCCAACACAGTCACTCATGAGGGGCCGAAGGCAATTCACAGTA 2340
XX |||
QY 3136 GGGGATCTCACTTCTGTATCAAGAGGGTCACTACTCTCCCGGCTTATAT 3195
XX |||
XX 2341 GGGGATCTCACTTCTGTATCAAGAGGGTCACTACTCTCCCGGCTTATAT 2400
XX |||
QY 3196 CCTATGACAGTCAAGCAAAACAGCCACTCTTCAATAGTCTTATACATTCATGCTTC 3255
XX |||
XX 2401 CCTATGACAGTCAAGCAAAACAGCCACTCTTCAATAGTCTTATACATTCATGCTTC 2460
XX |||
QY 3256 ACTGCGCAGGATGATTCCTTCCGAGGCTTCAGCAAGAGTCCCAACTGCTGTACT 3315
XX |||
XX 2461 ACTGCGCAGGATGATTCCTTCCGAGGCTTCAGCAAGAGTCCCAACTGCTGTACT 2520
XX |||
QY 3316 GAGTCTATACAGATCCATATCCCTATCTTCTATGAAGC 3358
XX |||
XX 2521 GAGTCTATACAGATCCATATCCCTATCTTCTATGAAGC 2563
XX |||
```

## RESULT 8

AA068943  
ID AA068943 standard; DNA; 4177 BP.

XX AA068943;

AC 25-MAR-2003 (revised)  
DT 13-APR-1995 (first entry)

XX SfiI fragment contg. Newcastle Disease Virus HN and F genes.

XX SfiI fragment; Newcastle Disease Virus; HN gene; F gene; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

XX FT 115..1860  
FT /tag= a

XX FT /label= AAR58859  
FT 2095..3756

XX FT /tag= b  
XX /label= AAR58858

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PN M09419014-A1.
XX
XX 01-SEP-1994.
XX
XX 28-FEB-1994; 94MO-US001826.
XX
XX 26-FEB-1993; 93US-00024156.
XX
XX (SYTR ) SYNPRO CORP.
XX (JAPR ) NIPPON ZEON KK.
XX
XX Cochran MD;
XX
XX WPI; 1994-294007/36.
XX P-PSDB; AAR58858, AAR58859.
XX
XX New recombinant fowl pox virus for use in vaccines - contains genes
XX expressing antigens of Newcastle disease virus and opt. infectious
XX bronchitis virus.
XX
XX Disclosure; Page 63-68; 85pp; English.
```

CC Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfiI  
CC fragment into the homology vector 443-88.8 at the unique SfiI site. The  
CC NDV HN and F genes were inserted in the same transcriptional orientation  
CC as the ORF in the parental homology vector. The sequence of SfiI fragment  
CC is in AA068943/R58858/AAR58859. The inserted SfiI fragment has the  
CC following structure: Junction A - Fragment 1 (HN, Aas 2-577) - Junction B  
CC - Fragment 2 (F, Aas 1-553) - Junction C - Fragment 3 (PBR322) - Junction  
CC D. Fragment 1 is approx. 1811 bp Availi to NaeI fragment of the NDV HN  
CC cDNA clone (BI strain). Fragment 2 is an approx 1812 bp BamHI to PstI  
CC fragment of the full length NDV F cDNA (BI Strain). Fragment 3 is an  
CC approx 235 bp PstI and SmaI fragment of the plasmid pBR322. The sequences  
CC of the junctions are in AA068945, AA068946, AA068947 and AA068948.  
XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.9%; Score 1741.8; DB 2; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
QY 16 TGAATCCCGGTTGGCGCCCTTCAGAGTSCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
XX |||
XX 2064 TGAATCCCGGTTGGCGCCCTTCAGAGTSCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
XX |||
QY 76 AGCACCTATGATGCTGACTATCCGGGTTGGCTGGCACTAGTGTGATCTGTCGGGCAA 135
XX |||
XX 2124 AGCACCTATGATGCTGACTATCCGGGTTGGCTGGCACTAGTGTGATCTGTCGGGCAA 2183
XX |||
QY 136 CTCGATTGATGGCAGGCGCTCTGACGCTGCAGGAATGTGGTTACAGAGCAAAAGCCGT 195
XX |||
XX 2184 CTCGATTGATGGCAGGCGCTCTGACGCTGCAGGAATGTGGTTACAGAGCAAAAGCAGT 2243
XX |||
QY 196 CAACATATACACCTCATCCAGACAGATCAATCATATGTTAAGTCTCCGAACTTGGC 255
XX |||
XX 2244 CAACATATACACCTCATCCAGACAGATCAATCATATGTTAAGTCTCCGAACTTGGC 2303
XX |||
QY 256 CAAGGATPAGAGGAGCATGTGGAAAGCCCTTGGATGATCAACAGAGATTTAGCACAC 315
XX |||
XX 2304 CAAGGATPAGAGGAGCATGTGGAAAGCCCTTGGATGATCAACAGAGATTTAGCACAC 2363
XX |||
QY 316 TTGGCTACCCCTTGGTGTGCTATCCGATGATCAAGAGCTGTGATCATCATCTGG 375
XX |||
XX 2364 TTGGCTACCCCTTGGTGTGCTATCCGATGATCAAGAGCTGTGATCATCATCTGG 2423
XX |||
QY 376 AGGGGGAGACAGGGGCGCTTATAGCGCCATTAATTTGGCGTGTGCTTTGGGTTGC 435
XX |||
XX 2424 AGGGGGAGACAGGGGCGCTTATAGCGCCATTAATTTGGCGTGTGCTTTGGGTTGC 2483
XX |||
QY 436 AACTGCGGACAAATTAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 495
XX |||
XX 2484 AACTGCGGACAAATTAACAGCGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 2543
XX |||
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QY	496	CATCTCCGACTTTAAAGAGATTGGCCGCAACAATAGAGGTGTGCATGAGGTCACTGA	555
Db	2544	CATCTCCGACTTTAAAGAGATTGGCCGCAACAATAGAGGTGTGCATGAGGTCACTGA	2603
QY	556	CGGATTTATCGCACTTAGCAGTGGCGATTGGAGAGTGCAGCAGTTTGTTAATGACCAAT	615
Db	2604	CGGATTTATCGCACTTAGCAGTGGCGATTGGAGAGTGCAGCAGTTTGTTAATGACCAAT	2663
QY	616	TAATTAACACCTCAGGAAATTAGATCGATCAAAATTGCAACGCAAGTTGGTGTAGACT	675
Db	2664	TAATTAACACCTCAGGAAATTAGATCGATCAAAATTGCAACGCAAGTTGGTGTAGACT	2723
QY	676	CAACCTGTACCTAACCGAATTGACTACAGTATTCCGACCACAAATCACTTCACTGCTTT	735
Db	2724	CAACCTGTACCTAACCGAATTGACTACAGTATTCCGACCACAAATCACTTCACTGCTTT	2783
QY	736	AAACAGCTGACTATTACGCACTTTACATCTAGCTGTGGAAATTGCAATTACTTATT	795
Db	2784	AAACAGCTGACTATTACGCACTTTACATCTAGCTGTGGAAATTGCAATTACTTATT	2843
QY	796	GACTAAGTTAGTGTAGGGAACAATCACTCAGCTACTTAATTCGGTAGCCGCTTAATCAG	855
Db	2844	GACTAAGTTAGTGTAGGGAACAATCACTCAGCTACTTAATTCGGTAGCCGCTTAATCAG	2903
QY	856	CGGTAAACCTTATCTATACGACTCAGACTCAACTCTTGGGTATACAGTAACTCTAAC	915
Db	2904	CGGTAAACCTTATCTATACGACTCAGACTCAACTCTTGGGTATACAGTAACTCTAAC	2963
QY	916	TTTCAGTCGGGGAACCTAAATTAATATGCGGCAACCTACCTTGGAAACCTTATCCGTAAAGAC	975
Db	2964	TTTCAGTCGGGGAACCTAAATTAATATGCGGCAACCTACCTTGGAAACCTTATCCGTAAAGAC	3023
QY	976	AACCAAGGGGAATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACAGTCCGTTCTGTAT	1035
Db	3024	AACCAAGGGGAATTTGGCTCGGCACTTGTCCCAAAAGTGTGACACAGTCCGTTCTGTAT	3083
QY	1036	AGAAAGACTTGACACCTCATACTGTATATGAAACTGACTTAATTTATATTTGTAACAAGAT	1095
Db	3084	AGAAAGACTTGACACCTCATACTGTATATGAAACTGACTTAATTTATATTTGTAACAAGAT	3143
QY	1096	AGTAACGTTCCCTATGTGTCCTCGGATTTTATTCCTGCTTGAGCGGCATTAAGTCGGACCTG	1155
Db	3144	AGTAACGTTCCCTATGTGTCCTCGGATTTTATTCCTGCTTGAGCGGCATTAAGTCGGACCTG	3203
QY	1156	TATGTACTCAAGAACGGAAGCGCACTTACTACACCATACATGACTATCAAGGTTCACT	1215
Db	3204	TATGTACTCAAGAACGGAAGCGCACTTACTACACCATACATGACTATCAAGGTTCACT	3263
QY	1216	CATGCGCAACCTGCAGATGACAACTGTATGTGTAAACCCCGGGGTATCATATGCGCA	1275
Db	3264	CATGCGCAACCTGCAGATGACAACTGTATGTGTAAACCCCGGGGTATCATATGCGCA	3323
QY	1276	AAACTATGAGAAGCCGTGTCTCTATATGATTAACATCATGCAATGTTTTATCCTTAGG	1335
Db	3324	AAACTATGAGAAGCCGTGTCTCTATATGATTAACATCATGCAATGTTTTATCCTTAGG	3383
QY	1336	CGGGTAACTTTAAGGGCTCAGTGGGGAAATTGCATGTAACTTATCAGAAAGATATCTCAAT	1395
Db	3384	CGGGTAACTTTAAGGGCTCAGTGGGGAAATTGCATGTAACTTATCAGAAAGATATCTCAAT	3443
QY	1396	ACAAGATTCTCAAGTAAATATTAACAGGAATCTTGAATATCAACTGACCTTGGGAATGT	1455
Db	3444	ACAAGATTCTCAAGTAAATATTAACAGGAATCTTGAATATCAACTGACCTTGGGAATGT	3503
QY	1456	CAACAACCTCGATCAGTAATATGCTTTGAAATTAAGTTAGAGGAAAGCAACAGAAAATTAGACAA	1515
Db	3504	CAACAACCTCGATCAGTAATATGCTTTGAAATTAAGTTAGAGGAAAGCAACAGAAAATTAGACAA	3563
QY	1516	AGTCAATGTCAAACTGACTATGACACTCTGCTCTCAATTACCTATATCGTTTGAAGTATCAT	1575
Db	3564	AGTCAATGTCAAACTGACTATGACACTCTGCTCTCAATTACCTATATCGTTTGAAGTATCAT	3623

QY	1576	ATCTCTGTTTGGTAACTTACCTAGCTGATTTCTACGATGCTACCTAAATGTATACAGCAAAA	163
DB	3684	ATCTCTGTTTGGTAACTTACCTAGCTGATTTCTACGATGCTACCTAAATGTATACAGCAAAA	368
QY	1636	GGCGCAACAAACAACTTATTATGCTTGGGAATATATCTTATGATCAGATGAGCCAC	169
DB	3684	GGCGCAACAAACAACTTATTATGCTTGGGAATATATCTTATGATCAGATGAGCCAC	374
QY	1686	TACAAAAATGTGAAACACAGATGAGGAAGAAAGGTTCCCTTAATATGATTTGTGAAAG	175
DB	3744	TACAAAAATGTGAAACACAGATGAGGAAGAAAGGTTCCCTTAATATGATTTGTGAAAG	380
QY	1756	TTCTGTAGTCTGTCTGATTCAGAGATTAGAAAAAA	1792
DB	3804	TTCTGTAGTCTGTCTGATTCAGAGATTAGAAAAAA	3840
RESULT 9			
AAQ70570			
ID	AAQ70570	standard; DNA; 4177 BP.	
XX			
AC	AAQ70570;		
XX			
DT	25-MAR-2003	(revised)	
DT	14-APR-1995	(first entry)	
XX			
DE	SfliI fragment contg. Newcastle disease virus HN and F genes.		
XX			
KM	Newcastle disease virus; HN gene; F gene; SfliI; vector 502-26.22; 95.		
XX			
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	115..1860	
FT		/*tag= a	
FT		/label= AAR58598, HN	
FT	CDS	2095..3756	
FT		/*tag= b	
FT		/label= AAR49141, F	
XX			
PN	MO9419015-A1.		
XX			
PD	01-SEP-1994.		
XX			
PF	28-FEB-1994;	94WO-US002252.	
XX			
PR	26-FEB-1993;	93US-00024156.	
XX			
PA	(SYTR ) SYNTRO CORP.		
XX			
PI	Cochran MD;		
XX			
DR	WPI; 1994-294008/36.		
XX			
XX	P-PSDB; AAR58598; AAR49141.		
PT	New recombinant fowl pox viruses - useful as vaccines against fowl pox		
PT	virus, Newcastle disease virus and infectious laryngotracheitis virus.		
XX			
PS	Disclosure; Page 72-77; 97pp; English.		
XX			
CC	AAQ70570 is the SfliI fragment insert in Homology Vector 502-26.22 contg.		
CC	Newcastle disease virus (NDV) HN and F genes. The structure of the		
CC	fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577) - Junction B		
CC	- Fragment 2 (NDV F AAs 1-553) - Junction C - Fragment 3 (PBR322) -		
CC	Junction D - 3'. Fragment 1 is Avail to NaeI fragment of the full length		
CC	NDV HN cDNA clone (BI strain). Fragment 2 is BamHI to PstI fragment of		
CC	the full length NDV F cDNA (BI strain). Fragment 3 is a PstI and ScaI		
CC	fragment of PBR322. The structures of the junctions A, B, C and D are		
CC	given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively. (Updated		
CC	on 25-MAR-2003 to correct PN field.)		
XX			
Q0	Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;		

Query Match		51.9%; Score 1741.8; DB 2; Length 4177;	
Best Local Similarity		98.8%; Pred. No. 0;	
Matches 1755; Conservative		0; Mismatches 22; Indels 0; Gaps 0;	
Qy	16	TGATATCCGGTGGCGCCCTCCAGATGAGATGGGCTCCAGACCTTCTACCAAGACC	75
Db	2064	TCGATCCCGGTGGCGCCCTCCAGATGAGATGGGCTCCAGACCTTCTACCAAGACC	2123
Qy	76	AGCACTATGATGTGATCTATCCGGGTTGCGCTGGCACTGAGTTGATCTGCCGCA	135
Db	2124	AGCACTATGATGTGATCTATCCGGGTTGCGCTGGCACTGAGTTGATCTGCCGCA	2183
Qy	136	CTCCATTGATGAGCGGCTCTTTCAGCTGAGAAATTTGGTTACAGAGACAAAGCCGT	195
Db	2184	CTCCATTGATGAGCGGCTCTTTCAGCTGAGAAATTTGGTTACAGAGACAAAGCCGT	2243
Qy	196	CAACATATACCTTCATCCAGACAGATCAATCATAGTTAAAGTCTCCCGGAATCTGCC	255
Db	2244	CAACATATACCTTCATCCAGACAGATCAATCATAGTTAAAGTCTCCCGGAATCTGCC	2303
Qy	256	CAAGATTAAGGAGGATGTGGAAAGCCCTTGGATCATACAACAGACATTGACAC	315
Db	2304	AAAGATTAAGGAGGATGTGGAAAGCCCTTGGATCATACAACAGACATTGACAC	2363
Qy	316	TTTGCTACCCCTTGGTGACTCTATCCGTAGATACAGAGTCTGTGACTACATCTGG	375
Db	2264	TTTGCTACCCCTTGGTGACTCTATCCGTAGATACAGAGTCTGTGACTACATCTGG	2423
Qy	376	AGGGGGAGACAGGGGCGCTTATAGCGGCAATATTGGCGTGTGCTTTGGGGTTGC	435
Db	2424	AGGGGGAGACAGGGGCGCTTATAGCGGCAATATTGGCGTGTGCTTTGGGGTTGC	2483
Qy	436	AACCTCCGCAAAATTAACAGGCGCGCAGCTCTGATTAAGCAAGCAAAATGTGCGCA	495
Db	2484	AACCTCCGCAAAATTAACAGGCGCGCAGCTCTGATTAAGCAAGCAAAATGTGCGCA	2543
Qy	496	CATCCTCCGACTTAAAGAGACATTTGCGCAACCAATAGGCTGTGATGAGTCACTGA	555
Db	2544	CATCCTCCGACTTAAAGAGACATTTGCGCAACCAATAGGCTGTGATGAGTCACTGA	2603
Qy	556	CGGATTAACGAACTAGACAGTGGCAATTGGGAAGATGACAGATTGTTAATGACAAAT	615
Db	2604	CGGATTAACGAACTAGACAGTGGCAATTGGGAAGATGACAGATTGTTAATGACAAAT	2663
Qy	616	TAAATAAACAGCTACAGAAATTTAGACTGCATCAAAATTTGCAACAGAAATTTGTAAGACT	675
Db	2664	TAAATAAACAGCTACAGAAATTTAGACTGCATCAAAATTTGCAACAGAAATTTGTAAGACT	2723
Qy	676	CAACCTGAACTTAACGAAATTTGATCAAGTATTCGAAACCAAAATCACTTCACTGCTTT	735
Db	2724	CAACCTGAACTTAACGAAATTTGATCAAGTATTTGGGACCAAAATCACTTCACTGCTTT	2783
Qy	736	AAACAAAGTGAATTTAGAGCACTTTTCAATCTAGCTGGTGGAAATATGATTAATT	795
Db	2784	AAACAAAGTGAATTTAGAGCACTTTTCAATCTAGCTGGTGGAAATATGATTAATT	2843
Qy	796	GACTTAAGTTAGGTAGGAAACAATCAACTGACTTAATTCGGTAGCGGCTTAATAC	855
Db	2844	GACTTAAGTTAGGTAGGAAACAATCAACTGACTTAATTCGGTAGCGGCTTAATAC	2903
Qy	856	CGGTAACCTTAATTTATACGACTCAAGACTCACTCTGGGTTATACAGTAACTTAC	915
Db	2904	CGGTAACCTTAATTTATACGACTCAAGACTCACTCTGGGTTATACAGTAACTTAC	2963
Qy	916	TTTCACTGGGAAACCTTAATTAATATGCGTGCACACTTACTTGGAAACCTTATCCGTAAAGCAC	975
Db	2964	TTTCACTGGGAAACCTTAATTAATATGCGTGCACACTTACTTGGAAACCTTATCCGTAAAGCAC	3023
Qy	976	AACCAAGGAGATTTGCTCGGACTTTGTCCAAAGGTGTGACACAGTGGTCTGTAT	1035
Db	3024	AACCAAGGAGATTTGCTCGGACTTTGTCCAAAGGTGTGACACAGTGGTCTGTAT	3083
Qy	1036	AGAAGAATTGACACCTCATCTGTATGAAACGACTTAATTAATTTGTAACAAGAT	1095

Db	3084	AGAAGAATTGACACCTCATCTGTATGAAACGACTTAAGTTTATTTGTAACAAGAT	3143
Qy	1096	AGTAACGTTCCCTATATGTCCTCCGTGATTTATTCCTGTGAGCGGCAATAGCTGGCCTG	1155
Db	3144	AGTAACGTTCCCTATATGTCCTCCGTGATTTATTCCTGTGAGCGGCAATAGCTGGCCTG	3203
Qy	1156	TATGTACTCAAAAGCCGAGCGCACTTATACACCATATGACTATCAAAAGTTTACGT	1215
Db	3204	TATGTACTCAAAAGCCGAGCGCACTTATACACCATATGACTATCAAAAGTTTACGT	3263
Qy	1216	CATGCCAACCTGCAAGATGACAAATGATGTAAGTGTAAACCCCGGGGTATCATATGCA	1275
Db	3264	CATGCCAACCTGCAAGATGACAAATGATGTAAGTGTAAACCCCGGGGTATCATATGCA	3323
Qy	1276	AAACTATGAGAAACCGGTCTCTAATATGATTAACAATCATGCAATGTTTATCTTAGG	1335
Db	3324	AAACTATGAGAAACCGGTCTCTAATATGATTAACAATCATGCAATGTTTATCTTAGG	3383
Qy	1336	CGGATTAACCTTAAAGGCTCAGTGGGAAATTTGATGTAACTTATCAAGAAATATCTCAAT	1395
Db	3384	CGGATTAACCTTAAAGGCTCAGTGGGAAATTTGATGTAACTTATCAAGAAATATCTCAAT	3443
Qy	1396	ACAAGATTTCTAAGTAAATTAACAAGCAATCTTGATATCTCACTGAGCTTGGGAATGT	1455
Db	3444	ACAAGATTTCTAAGTAAATTAACAAGCAATCTTGATATCTCACTGAGCTTGGGAATGT	3503
Qy	1456	CAACAACCTGATTCAGTAAATGTTGAATTAAGTTAGGAAAGCAACAGAAACTAGACAA	1515
Db	3504	CAACAACCTGATTCAGTAAATGTTGAATTAAGTTAGGAAAGCAACAGAAACTAGACAA	3563
Qy	1516	AGTCAATGTCAAACTGATACACATCTGCTCTGATTAACCTATATCGTTTGAATATCAT	1575
Db	3564	AGTCAATGTCAAACTGATACACATCTGCTCTGATTAACCTATATCGTTTGAATATCAT	3623
Qy	1576	ATCTCTGTTTGGTATTAATGATCTGATTTGATGATGCTTACCTTAATGTAACAGCAAA	1635
Db	3624	ATCTCTGTTTGGTATTAATGATCTGATTTGATGATGCTTACCTTAATGTAACAGCAAA	3683
Qy	1636	GGCGCAACAAAAACCTTATATGAGCTTTGGAAATATATCTAGTCAATGAGAGCCAC	1695
Db	3684	GGCGCAACAAAAACCTTATATGAGCTTTGGAAATATATCTAGTCAATGAGAGCCAC	3743
Qy	1696	TACAAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTAATATGTAATTTGTGAAG	1755
Db	3744	TACAAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTAATATGTAATTTGTGAAG	3803
Qy	1756	TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA	1792
Db	3804	TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA	3840
RESULT 10			
AAT48510			
ID AAT48510 standard; DNA; 4177 BP.			
XX			
AC AAT48510;			
XX			
DT 05-MAY-1997 (first entry)			
XX			
DE Sfil fragment encoding Newcastle disease virus HN and F genes.			
XX			
KM Fowlpox virus; PPV, recombinant virus; vector: vaccine; immunisation;			
KM Newcastle disease virus; NDV; haemagglutinin; fusion protein; poultry;			
KM ds.			
OS Newcastle disease virus.			
XX			
FH Key			
FH CDS			
FH Location/Qualifiers			
FH 115..1860			
FH /tag= a			
FH /product= "NDV haemagglutinin"			
FH FT			
FT CDS			
FT 2095..3756			



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FT      /*tag= b
FT      /product= "NDV fusion protein"
PN      MO640880-A1.
XX      19-DEC-1996.
PD      04-JUN-1996; 96WO-US011187.
XX      07-JUN-1995; 95US-00484790.
XX      (SYTR ) SYNTRO CORP.
XX      Cochran MD, Junker DE, Singer PA;
PI      WPI; 1997-087060/08.
DR      P-PSDB; AAM10690, AAM10691.
XX      New recombinant fowlpox virus - contg. a foreign DNA sequence inserted
PT      into the fowlpox virus genome, used for the produ. of vaccines.
XX      Disclosure; Page 102-107; 134pp; English.
XX      An SfiI fragment (AAT48510), contg. coding sequences for Newcastle
CC      disease virus (NDV) haemagglutinin (HN) (AAM10690) and fusion protein (F)
CC      (AAM10691), was inserted into homology vector 443-88.8 (see also
CC      AAT48511) at the unique SfiI site, yielding homology vector 502-26.22
CC      (see also AAT48502-05). The NDV HN and F genes were inserted in the same
CC      transcriptional orientation as the parental homology vector. 502-26.22
CC      was used to insert the NDV HN and F genes into fowlpox virus. The
CC      resulting recombinant virus can be used to deliver the vaccine antigens
CC      to poultry.
XX      Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
SQ      Query Match 51.9%; Score 1741.8; DB 2; Length 4177;
        Best Local Similarity 98.8%; Pred. No. 0;
        Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
        Query      16  TGGATCCCGGTTGGCGGCTTCAGAGTGAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
        Db         2064  TCGATCCCGGTTGGCGGCTTCAGAGTGAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
        QY          76  AGCACTATGATGCTGACTATCCGGGTTGCGCTGSCACTGAGTGCATCTGTCCGGCAAA 135
        Db         2124  AGCACTATGATGCTGACTATCCGGGTTGCGGCTGCTGTAAGTGCATCTGTCCGGCAAA 2183
        QY          136  CTCGATTGATGGCGAGGCTCTTTCAGCTGCAGGAATTGTGTTACAGAGACAAAGCCGT 195
        Db         2184  CTCGATTGATGGCGAGGCTCTTTCAGCTGCAGGAATTGTGTTACAGAGACAAAGCAAT 2243
        QY          196  CAACATATACACCTCATCCAGACAGAGATCAATCATGTTAAGTCCGCCGGAATCTGCC 255
        Db         2244  CAACATATACACCTCATCCAGACAGAGATCAATCATGTTAAGTCCGCCGGAATCTGCC 2303
        QY          256  CAAGATTAAGAGGATGTCGGAAGGCCCTTTCAGATGATACAAAGCAATTGACAC 315
        Db         2304  AAAGGATTAAGAGGATGTCGGAAGGCCCTTTCAGATGATACAAAGCAATTGACAC 2363
        QY          316  TTTTGCTCACCCCCTTGGTGACTCTATCCGTAAGATCAAGAGTCTGTGACTACATCTGG 375
        Db         2364  TTTTGCTCACCCCCTTGGTGACTCTATCCGTAAGATCAAGAGTCTGTGACTACATCTGG 2423
        QY          376  AGGGGGGAGACAGGGGGGCTTTATAGGCGCATTAATTGGGGTGCTCTTGGGGTTGC 435
        Db         2424  AGGGGGGAGACAGGGGGGCTTTATAGGCGCATTAATTGGGGTGCTCTTGGGGTTGC 2483
        QY          436  AACTGCGCAAAATTAACAGCGCGCAGCTCTGTATCAAGCCAAAGAAATGCTGCCAA 495
        Db         2484  AACTGCGCAAAATTAACAGCGCGCAGCTCTGTATCAAGCCAAAGAAATGCTGCCAA 2543
        QY          496  CATCTCCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 555
        Db         |||
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Db         2544  CATCTCCGACTTAAAGAGACATTTGCCGCAACCAATGAGGCTGTGCATGAGTCACTGA 2603
QY          556  CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGCAGACGTTTGTAAATGCAAT 615
Db         2604  CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGCAGACGTTTGTAAATGCAAT 2663
QY          616  TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTTGCACAGCAATTTGGTGAAGCT 675
Db         2664  TAATTAACAGCTCAGGAATTTAGCTGCATCAAAATTTGCACAGCAATTTGGTGAAGCT 2723
QY          676  CAACCTGTACTTAACGAATTTGACTACAGTATTCGAGCAACAAATCACTTCACTGCTTT 735
Db         2724  CAACCTGTACTTAACGAATTTGACTACAGTATTCGAGCAACAAATCACTTCACTGCTTT 2783
QY          736  AAACAAGCTGACTATTACAGGACCTTTTAACTAGCTGTGGAATAATGATTAATTAAT 795
Db         2784  AAACAAGCTGACTATTACAGGACCTTTTAACTAGCTGTGGAATAATGATTAATTAAT 2843
QY          796  GACTAATTAGGTGTAGGGAACAATCACTCAGCTCTTAATGCGTAGCGGCTTAATCAC 855
Db         2844  GACTAATTAGGTGTAGGGAACAATCACTCAGCTCTTAATGCGTAGCGGCTTAATCAC 2903
QY          856  CGGTAACCTTATCTATAGACTCAGAGCTCAAGCTCAACTCTTGGGTTACAGGTAACCT 915
Db         2904  CGGTAACCTTATCTATAGACTCAGAGCTCAAGCTCAACTCTTGGGTTACAGGTAACCT 2963
QY          916  TTCAGTGGGAACCTTAATTAATATGCTGCGACCTTCTTGGAACCTTATCCGTAGCAC 975
Db         2964  TTCAGTGGGAACCTTAATTAATATGCTGCGACCTTCTTGGAACCTTATCCGTAGCAC 3023
QY          976  AACCAAGGGAATTTGCTCCGCGACCTTTCGCAAAAGTGTGACACAGGTCGGTTCGTGAT 1035
Db         3024  AACCAAGGGAATTTGCTCCGCGACCTTTCGCAAAAGTGTGACACAGGTCGGTTCGTGAT 3083
QY          1036  AGAAGAACTTGAACACCTCATAGTATAGAACTGACTTATGATTTATTTATGTCAGAAAT 1095
Db         3084  AGAAGAACTTGAACACCTCATAGTATAGAACTGACTTATGATTTATTTATGTCAGAAAT 3143
QY          1096  AGTAACGTTCCATATGTCCTGTTATTTATTCCTGCTTGAAGCGGCAATACGTGCGCTG 1155
Db         3144  AGTAACGTTCCATATGTCCTGTTATTTATTCCTGCTTGAAGCGGCAATACGTGCGCTG 3203
QY          1156  TATGTACTCAAGAAGCGAAGCGGCACTTACTACCATATCATGATCTTCAAAGGTTCAAT 1215
Db         3204  TATGTACTCAAGAAGCGAAGCGGCACTTACTACCATATCATGATCTTCAAAGGCTCAAT 3263
QY          1216  CATGCGCAATGGAAGTGAACAATGATGATGTAAACCCCGGGGTATCATATGCA 1275
Db         3264  CATGCGCAATGGAAGTGAACAATGATGATGTAAACCCCGGGGTATCATATGCA 3323
QY          1276  AAACATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCAATGTTTATCTTAGG 1335
Db         3324  AAACATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCAATGTTTATCTTAGG 3383
QY          1336  CGGGATTACTTTAAGGCTCAGTGGGGAAATTCAGATGTAATCTTATCAGAAATATCTCAAT 1395
Db         3384  CGGGATTACTTTAAGGCTCAGTGGGGAAATTCAGATGTAATCTTATCAGAAATATCTCAAT 3443
QY          1396  ACAAGATTCCTCAAGTATTAATAACAGCAATCTTGATATCTCAACGAGGTTGGGAATGT 1455
Db         3444  ACAAGATTCCTCAAGTATTAATAACAGCAATCTTGATATCTCAACGAGGTTGGGAATGT 3503
QY          1456  CAACAACCTGATCAGTAATCTTTGAATAAGTTAGAGAAAGCAACAGAAATCTAGCAA 1515
Db         3504  CAACAACCTGATCAGTAATCTTTGAATAAGTTAGAGAAAGCAACAGAAATCTAGCAA 3563
QY          1516  AGTCAATGTCAAACTGATAGCAATCTGCTCATTAATCTATATCTTTGACTATCAT 1575
Db         3564  AGTCAATGTCAAACTGATAGCAATCTGCTCATTAATCTATATCTTTGACTATCAT 3623
QY          1576  ATCTCTGTTTTTGGTATTAATTTAGCCGTGATTCAGAGATGCTACTAATGTAAGCAAAA 1635
Db         3624  ATCTCTGTTTTTGGTATTAATTTAGCCGTGATTCAGAGATGCTACTAATGTAAGCAAAA 3683
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QY 1636 GGGCGCAACAAAAACCTTATTATGGCTTGGGAATTAATCTTAGATGATGAGAGCCAC 1695
DB 3684 GGGCGCAACAAAAACCTTATTATGGCTTGGGAATTAATCTTAGATGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACACAGATGAGGAAAGGTTTCCCTTAATAGTAAATTTGTGTGAAG 1755
DB 3744 TACAAAAATGTGAACACAGATGAGGAAAGGTTTCCCTTAATAGTAAATTTGTGTGAAG 3803
QY 1756 TTCTGGTAGTCTGTCACTTCAAGAGTTAAGAAAAA 1792
DB 3804 TTCTGGTAGTCTGTCACTTCAAGAGTTAAGAAAAA 3840

RESULT 11
AAx81147
ID AAx81147 standard; DNA; 4177 BP.
XX
AC AAx81147;
XX
DT 07-SEP-1999 (first entry)
XX
DE Seq ID No: 12 of US5925358.
XX
KM Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
XX Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis; ds.
XX
OS Fowlpox virus.
XX
FH Key Location/Qualifiers
FT CDS 115..1860
FT FT /*tag= a
FT CDS 2095..3756
FT FT /*tag= b

US5925358-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00484575.
XX
PR 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94MO-US002252.
XX
PA (SYTR ) SYNTHRO CORP.
XX
PI Junker DE, Cochran MD;
XX
DR WPI; 1999-418249/35.
XX
DR P-PSDB; AAY21982, AAY21983.
XX
PT Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX
PS Disclosure; Col 61-70; 108pp; English.
XX
CC The invention relates to a recombinant fowlpox virus (FPV) comprising a
CC foreign DNA inserted into a region of the fowlpox virus genome
CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
CC host cell. The virus is used as a vaccine for immunising chickens against
CC Newcastle disease virus (NDV), Fowlpox, and infectious laryngotracheitis
XX
SQ Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
Query Match 51.9%; Score 1741.8; DB 2; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 16 TGAATCCCGGTTGGCCCTCCAGATGCAAGATGGCTCCAGACCTTACCAAGAACCC 75
DB 2064 TCGATCCCGGTTGGCCCTCCAGATGCAAGATGGCTCCAGACCTTACCAAGAACCC 2123
QY 76 AGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGATTGCACTCTGTCCGGCAAA 135
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DB 2124 AGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGATTGCACTCTGTCCGGCAAA 2183
QY 136 CTCATTTGATGCAAGGCTCTTTCAGCTGCAAGAAATTTGTGTTACAGAGACAAGCCGT 195
DB 2184 CTCATTTGATGCAAGGCTCTTTCAGCTGCAAGAAATTTGTGTTACAGAGACAAGCAAGT 2243
QY 196 CAACATTTACACCTCATCCAGACAGATCAATATATGTTTAAGTCTCTCCGAAATCTGCC 255
DB 2244 CAACATTTACACCTCATCCAGACAGATCAATATATGTTTAAGTCTCTCCGAAATCTGCC 2303
QY 256 CAAGATTAAGAGGCAATGCGAAAGCCCTTGATGATACAGACAGACATTTGACAC 315
DB 2304 AAAGATTAAGAGGCAATGCGAAAGCCCTTGATGATACAGACAGACATTTGACAC 2363
QY 316 TTTCCTACCCCTTTCAGCTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTCG 375
DB 2364 TTTCCTACCCCTTTCAGCTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTCG 2423
QY 376 AGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGCTTGC 435
DB 2424 AGGGGAGACAGGGGCGCTTATAGCGCCATTTATGGCGGTGGCTCTTGGGCTTGC 2483
QY 436 AACGCGGCAAAATAACAGGGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 495
DB 2484 AACGCGGCAAAATAACAGGGCGCGAGCTGTGATCAAGCCAAACAAATGCTGCCAA 2543
QY 496 CATCCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCGTGTGACATCTGA 555
DB 2544 CATCCTCCGACTTAAAGAGACATTTGCGCAACCAATGAGCGTGTGACATCTGA 2603
QY 556 CGGATTATCGCACTAGCAGTGGGAGATTTGGGAGATGACAGATTTGTTATGACCAAT 615
DB 2604 CGGATTATCGCACTAGCAGTGGGAGATTTGGGAGATGACAGATTTGTTATGACCAAT 2663
QY 616 TAAATAAAGCTCAGGAATTTAGCTGCATCAAAATTTGACAGAGATTTGTTAGAGCT 675
DB 2664 TAAATAAAGCTCAGGAATTTAGCTGCATCAAAATTTGACAGAGATTTGTTAGAGCT 2723
QY 676 CAACCTGACCTAACCGAATTTGACTAGTATTCGACCAACAAATCACTTCACTGCTTT 735
DB 2724 CAACCTGACCTAACCGAATTTGACTAGTATTTGGACCAACAAATCACTTCACTGCTTT 2783
QY 736 AACCAAGCTGACTATTCAGGACCTTTAACAATCTAGCTGTGGAATAATGATTAATTT 795
DB 2784 AACCAAGCTGACTATTCAGGACCTTTAACAATCTAGCTGTGGAATAATGATTAATTT 2843
QY 796 GACTAAGTTAGGTGAGGAAACAATCAACTAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
DB 2844 GACTAAGTTAGGTGAGGAAACAATCAACTAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903
QY 856 CGGTAACCTTATTCATACGCTCAGACACTCACTCTGGGGTTATACAGTAACCTTACC 915
DB 2904 CGGTAACCTTATTCATACGCTCAGACACTCACTCTGGGGTTATACAGTAACCTTACC 2963
QY 916 TTCAGTGGGAACTTAATATATATGCGTCCACTTCTTGAAACCTTATCCGTAAGCAC 975
DB 2964 TTCAGTGGGAACTTAATATATATGCGTCCACTTCTTGAAACCTTATCCGTAAGCAC 3023
QY 976 AACCAAGGATTTGCTCGGCACTTTCGCCAAAGTGTGACACAGTCCGTTCTGTAT 1035
DB 3024 AACCAAGGATTTGCTCGGCACTTTCGCCAAAGTGTGACACAGTCCGTTCTGTAT 3083
QY 1036 AGAAGACTTGACACTCATCTGATAGAAACTGACTTAGATTATTTATACAAAGAT 1095
DB 3084 AGAAGACTTGACACTCATCTGATAGAAACTGACTTAGATTATTTATACAAAGAT 3143
QY 1096 AGTAACGTTCCCTATGTCCCTGCTGATTTATTCCTGTGACGCGCAATACGTCGCTG 1155
DB 3144 AGTAACGTTCCCTATGTCCCTGCTGATTTATTCCTGTGACGCGCAATACGTCGCTG 3203
QY 1156 TATGTACTCAAAAGCCGAGGCGCACTTATACCATATCATATGACTATCAAAAGTTGAGT 1215
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Db 3204 TATGTACTCAAAAGCCGAGGCGCACTTACTACACCATATATGACTATCAAAAGGCTCACT 3263
Qy 1216 CATCGCCAACTGCAGAGATGACACACATGTAGATGTGTAAACCCCGGGTATCATATGCA 1275
Db 3264 CATCGCTAACTGCAGAGATGACACACATGTAGATGTGTAAACCCCGGGTATCATATGCA 3323
Qy 1276 AAATCTATGAGAGAGCCGTGTCTTAAATGATTAACATCATGCAATGTTTATCTTAAAG 1335
Db 3324 AAATCTATGAGAGAGCCGTGTCTTAAATGATTAACATCATGCAATGTTTATCTTAAAG 3383
Qy 1336 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGATGTACTATGAGAAGATATCTCAAT 1395
Db 3384 CGGGATTAACCTTTAAGGCTCAGTGGGGAATTGATGTACTATGAGAAGATATCTCAAT 3443
Qy 1396 ACAAGATTCTCAAGTAAATTAATACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGT 1455
Db 3444 ACAAGATTCTCAAGTAAATTAATACAGGCAATCTTGATATCTCAACTGAGCTTGGAAATGT 3503
Qy 1456 CAACAACTCGATCGATTAATGCTTTGAATTAAGTTAGAGAAAGCAACGAAAACTAGACAA 1515
Db 3504 CAACAACTCGATCGATTAATGCTTTGAATTAAGTTAGAGAAAGCAACGAAAACTAGACAA 3563
Qy 1516 AGTCAATGTCAAACTGACATGCAATGCTCTGATTAACCTATACCTATGCTTTGACTATCAT 1575
Db 3564 AGTCAATGTCAAACTGACATGCAATGCTCTGATTAACCTATACCTATGCTTTGACTATCAT 3623
Qy 1576 ATCTCTGTTTGGTATTAATGCTTGAATCTGATTAAGTCTGATTAAGTCTGATTAAGTCTG 1635
Db 3624 ATCTCTGTTTGGTATTAATGCTTGAATCTGATTAAGTCTGATTAAGTCTGATTAAGTCTG 3683
Qy 1636 GGGGCAACAAAAACCTTATTAATGCTTGGGAATTAATCTGATTAAGTCTGATTAAGTCTG 1695
Db 3684 GGGGCAACAAAAACCTTATTAATGCTTGGGAATTAATCTGATTAAGTCTGATTAAGTCTG 3743
Qy 1696 TACAAAATGTGAACACAGATGAAGAAAGTTTCCCTTAATGATTAATGCTGATTAAGTCTG 1755
Db 3744 TACAAAATGTGAACACAGATGAAGAAAGTTTCCCTTAATGATTAATGCTGATTAAGTCTG 3803
Qy 1756 TTCTGTAGTCTGTCACTGATTAAGTCTGATTAAGTCTGATTAAGTCTGATTAAGTCTG 1792
Db 3804 TTCTGTAGTCTGTCACTGATTAAGTCTGATTAAGTCTGATTAAGTCTGATTAAGTCTG 3840

RESULT 12
AAZ49295
ID AAZ49295 standard; cDNA; 4177 BP.
XX
AC AAZ49295;
XX
DT 14-MAR-2000 (first entry)
XX
DE cDNA encoding NDV haemagglutinin-neuraminidase and fusion proteins.
XX
KW Fowlpox virus; FPV; recombinant; antigenic protein; expression;
KW Infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
KW Marek's disease virus; cytokine; promoter; homologous recombination;
KW homology vector; multivalent; live vaccine; haemagglutinin;
KW neuraminidase; fusion protein; ds.
XX
OS Newcastle disease virus.
XX
FH Key 115..1860
FT CDS /tag= a
FT CDS /product= "Haemagglutinin-neuraminidase (HN, AAY58182)"
FT CDS /tag= b
FT CDS /product= "Fusion (F) protein (AAY58183)"
XX
US6001369-A.
XX
PD 14-DEC-1999.
XX
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PF 07-JUN-1995; 95US-00477459.
XX
PR 26-FEB-1993; 93US-00024156.
PR 28-FEB-1994; 94MO-US002252.
XX
PA (SYNTR) SYNTR CORP.
XX
PI Junken DE, Cochran MD;
XX
DR MPI; 2000-071638/06.
DR P-PSDB; AAY58182, AAY58183.
XX
PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl against
PT Marek's disease, Newcastle disease, Infectious laryngotracheitis virus
PT and/or fowlpox.
XX
PS Claim 5; Col 61-68; 56pp; English.
XX
CC The invention relates to a recombinant fowlpox virus (FPV) comprising a
CC foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus
CC genome. The foreign DNA is capable of being expressed in a host cell into
CC which the fowlpox virus has been introduced and encodes an antigenic
CC protein. The antigenic protein which may be expressed includes infectious
CC laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD,
CC AAY58184), Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or
CC fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The
CC foreign DNA may alternatively encode a cytokine such as chicken
CC melanomacrocyclic growth factor (CMGF) or chicken interferon (CINF). The
CC foreign DNA in the recombinant FPV is under the control of one or more
CC synthetic pox promoters, enabling control of strength and timing of
CC heterologous gene expression. The synthetic pox virus promoters that may
CC be used are based on promoters of the vaccinia virus and include early
CC promoter 1 (EP1), late promoter 1 (LP1), EP2 and LP2 (AAZ49291-249294,
CC respectively). The recombinant FPV is generated via homologous
CC recombination between FPV DNA and a homology vector containing the
CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
CC the invention are used as multivalent live vaccines for immunising fowl
CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
CC present sequence represents cDNA encoding NDV haemagglutinin-
CC neuraminidase (HN) and fusion (F) proteins
XX
SQ Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTTGGCGGCTTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
Db 2064 TCGATCCCGGTTGGCGGCTTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
Qy 76 AGCACCTATGATCTGATCTGATCCGGGTTGGCTGCGCATGATGCTGTCCGGCAAA 135
Db 2124 AGCACCTATGATCTGATCTGATCCGGGTTGGCTGCGCATGATGCTGTCCGGCAAA 2183
Qy 136 CTCATTTGATGAGGAGGCTTCTTCACTGAGTGAATTTGGTTTACAGAGACAAAGCCGT 195
Db 2184 CTCATTTGATGAGGAGGCTTCTTCACTGAGTGAATTTGGTTTACAGAGACAAAGCAGT 2243
Qy 196 CAACATATACCTCTATCCACAGACAGATTAATCATATGATTAAGTCTCTCCGAATCTGCC 255
Db 2244 CAACATATACCTCTATCCACAGACAGATTAATCATATGATTAAGTCTCTCCGAATCTGCC 2303
Qy 256 CAAGGATTAAGGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315
Db 2304 CAAGGATTAAGGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3263
Qy 316 TTGTCTCAACCCCTTGTGATCTCTATCCGTAGATTAACAAGAGTCTGTGACTACATCTGG 375
Db 2364 TTGTCTCAACCCCTTGTGATCTCTATCCGTAGATTAACAAGAGTCTGTGACTACATCTGG 2423
Qy 376 AGGGGGGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 435
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Db 2124 AGGGGGGAGACAGGGGCGCTTATAGGGCCATTAATGCGGTGTGCTCTTGCGGTTTC 2483  
Qy 436 AACTGCCGACAAATTAACAGGCGCGCAGCTCTGATACAGCAAAACAAATGTCCGA 495  
Db 2484 AACTGCCGACAAATTAACAGGCGCGCAGCTCTGATACAGCAAAACAAATGTCCGA 2543  
Qy 496 CATCTCCGACTTAAAGAGACATTTGCCGAACCAATGAGGCTGTGATGAGTCACTGA 555  
Db 2544 CATCTCCGACTTAAAGAGACATTTGCCGAACCAATGAGGCTGTGATGAGTCACTGA 2603  
Qy 556 CGGATTTTCGACATGACAGTGGCAGTTGGGAAGATGACAGATTTGTTATGACCAAT 615  
Db 2604 CGGATTTTCGACATGACAGTGGCAGTTGGGAAGATGACAGATTTGTTATGACCAAT 2663  
Qy 616 TAATTAACACAGCTCAGAAATTAAGACTGATCAAAATTCACAGCAAGTTGGTGAAGCT 675  
Db 2664 TAATTAACACAGCTCAGAAATTAAGACTGATCAAAATTCACAGCAAGTTGGTGAAGCT 2723  
Qy 676 CAACCTGTACTTAAACGAAATTAAGACTGATCAAAATTCACAGCAAGTTGGTGAAGCT 735  
Db 2724 CAACCTGTACTTAAACGAAATTAAGACTGATCAAAATTCACAGCAAGTTGGTGAAGCT 2783  
Qy 736 AAACACAGCTGATTTACAGCACTTTACATCTAGCTGTGGAATATGATTAATTT 795  
Db 2784 AAACACAGCTGATTTACAGCACTTTACATCTAGCTGTGGAATATGATTAATTT 2843  
Qy 796 GACTAAGTTAGGTAGGGAACATCACTAGCTCAATTAACGCTTACGCTTAATGAC 855  
Db 2844 GACTAAGTTAGGTAGGGAACATCACTAGCTCAATTAACGCTTACGCTTAATGAC 2903  
Qy 856 CGGTACCCCTATTTCTATACAGCTCAACAGCTCAACTCTTGGGTATACAGTAACTTACC 915  
Db 2904 CGGTACCCCTATTTCTATACAGCTCAACAGCTCAACTCTTGGGTATACAGTAACTTACC 2963  
Qy 916 TTCAGTGGGAACTTAATTAATGCGGCCAAGCTTCTTGGAAACCTTATCCGTAAAGAC 975  
Db 2964 TTCAGTGGGAACTTAATTAATGCGGCCAAGCTTCTTGGAAACCTTATCCGTAAAGAC 3023  
Qy 976 AACCAAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGTCCGTCTGTAT 1035  
Db 3024 AACCAAGGGGATTTGCTCGGCACTTGTGTCCCAAAAGTGTGACACAGTCCGTCTGTAT 3083  
Qy 1036 AGAAGAACTTGACACCTCATCTGATAGAACTGACTTAATTTATTTGATACAGAT 1095  
Db 3084 AGAAGAACTTGACACCTCATCTGATAGAACTGACTTAATTTATTTGATACAGAT 3143  
Qy 1096 AGTAACGTTCCCTATGTCCTCGTATTTATTTCTGCTTGAAGCGCAATACGTGGCTG 1155  
Db 3144 AGTAACGTTCCCTATGTCCTCGTATTTATTTCTGCTTGAAGCGCAATACGTGGCTG 3203  
Qy 1156 TATGTACTCAAAAGCCGAGGCGCACTTACACCAATGACTATCAAAAGGTTCACT 1215  
Db 3204 TATGTACTCAAAAGCCGAGGCGCACTTACACCAATGACTATCAAAAGGTTCACT 3263  
Qy 1216 CATGCCAACTGCAAGATGACACATGATGATGTAACCCCGGGGTATCATATCGCA 1275  
Db 3264 CATGCCAACTGCAAGATGACACATGATGATGTAACCCCGGGGTATCATATCGCA 3323  
Qy 1276 AAATCTAGAGAGCCGTGTCTTAATGATTAACATCATGCAATGTTTATCTTAAAG 1335  
Db 3324 AAATCTAGAGAGCCGTGTCTTAATGATTAACATCATGCAATGTTTATCTTAAAG 3383  
Qy 1336 CGGATTAATTTAAGGCTCAGTGGGGAATTTGATGTAATTTACAGAAATATCTCAAT 1395  
Db 3384 CGGATTAATTTAAGGCTCAGTGGGGAATTTGATGTAATTTAAGAAATATCTCAAT 3443  
Qy 1396 ACAAGATTTCTCAAGTAATTAACAGCAATCTTGAATTCACACTGAGCTTGGGAATGT 1455  
Db 3444 ACAAGATTTCTCAAGTAATTAACAGCAATCTTGAATTCACACTGAGCTTGGGAATGT 3503  
Qy 1456 CAACCACTGATCAATTAATGCTTTGAATTAAGTAAAGAAAGCAACAGAAACTAGACAA 1515  
Db 3504 CAACCACTGATCAATTAATGCTTTGAATTAAGTAAAGAAAGCAACAGAAACTAGACAA 3563

Qy 1516 AGTCATGTCAAACATGACTAGACATCTGCTCTCATTAACCTAATGCTTTGACTATCAT 1575  
Db 3564 AGTCATGTCAAACATGACTAGACATCTGCTCTCATTAACCTAATGCTTTGACTATCAT 3623  
Qy 1576 ATCTCTGTTTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635  
Db 3624 ATCTCTGTTTTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3683  
Qy 1636 GGGCAACAAACAACTTATTAATGAGCTTGGGAATTAATTAATTAATTAATTAATTAATTAAT 1695  
Db 3684 GGGCAACAAACAACTTATTAATGAGCTTGGGAATTAATTAATTAATTAATTAATTAATTAAT 3743  
Qy 1696 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTAATAGTAATTTGTGAAAG 1755  
Db 3744 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTAATAGTAATTTGTGAAAG 3803  
Qy 1756 TTCTGTAGTCTGTCACTTCAAGAGTTTAAAGAAAAA 1792  
Db 3804 TTCTGTAGTCTGTCACTTCAAGAGTTTAAAGAAAAA 3840

## RESULT 13

AAC67862 standard; DNA; 4177 BP.

AAC67862;

06-AUG-2003 (revised)  
02-MAR-2001 (first entry)

Sfil1 fragment comprising NDV HN and F genes.

Fowlpox virus; FPV; antiviral; antibacterial; vaccine;  
Newcastle's disease virus; NDV; Marek's disease;  
infectious laryngotracheitis; Sfil1 fragment; HN glycoprotein;  
F glycoprotein; ds.

Newcastle disease virus.

US6136318-A.

24-OCT-2000.

07-JUN-1995; 95US-00486414.

26-FEB-1993; 93US-00024156.  
28-FEB-1994; 94WO-US002252.

(JUNK//) JUNKER D E.

(COCH//) COCHRAN M D.

Cochran MD, Junker DE;

WPI; 2000-686071/67.  
P-PSDB; AAB36038.New recombinant fowlpox virus useful as vaccines contains foreign DNA  
inserted into specific non-essential region of the genome.

Disclosure; Col 59-68; 56pp; English.

The present sequence is provided in a specification relating to a  
recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted  
within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA  
can be expressed in host cells infected with FPV. The recombinant FPV may  
be used in vaccines to protect animals (especially chickens) against  
fowlpox and, depending on the source of the foreign DNA, other diseases,  
particularly Newcastle's disease, Marek's disease or infectious  
laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

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Query Match      51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGAATCCCGGTTGGCGCCCTCAGATGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
DB 2064 TCGATCCCGGTTGGCGCCCTCAGATGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
QY 76 AGCACTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 135
DB 2124 AGCACTATGATGCTGATCTATCCGGGTTGGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 2183
QY 136 CTCATTGATGAGCGGCTCTTGCACTGCAAGAAATTGGTTTCAAGAGCAAAAGCCGT 195
DB 2184 CTCATTGATGAGCGGCTCTTGCACTGCAAGAAATTGGTTTCAAGAGCAAAAGCAAT 2243
QY 196 CAACATATACACCTATCCCAAGAGATCAATGTTAAAGTCCCTCCGAATCTGCC 255
DB 2244 CAACATATACACCTATCCCAAGAGATCAATGTTAAAGTCCCTCCGAATCTGCC 2303
QY 256 CAAGATTAAGAGGATGTGCGAAAGCCCTTGATGATATCAACAGACATTGACAC 315
DB 2304 AAAGATTAAGAGGATGTGCGAAAGCCCTTGATGATATCAACAGACATTGACAC 2363
QY 316 TTGCTCACTCCCTTGGTGACTCTATCCGTAAGATACAGAGTCTGTGACTCATCTGG 375
DB 2364 TTGCTCACTCCCTTGGTGACTCTATCCGTAAGATACAGAGTCTGTGACTCATCTGG 2423
QY 376 AGGGGGGAGACAGGGGGGCTTATAGGGCCATTAATGGGGGATGGGCTCTGGGGTTGC 435
DB 2424 AGGGGGGAGACAGGGGGGCTTATAGGGCCATTAATGGGGGATGGGCTCTGGGGTTGC 2483
QY 436 AACTGCCGCACAATAACAGGGGCGGAGCTCTGATACAAAGCCAAATGCTGCCAA 495
DB 2484 AACTGCCGCACAATAACAGGGGCGGAGCTCTGATACAAAGCCAAATGCTGCCAA 2543
QY 496 CATCTCCGACTTAAGAAGACATTTGCCGCAACCAAGAGCTGTGATGAGTCACTGA 555
DB 2544 CATCTCCGACTTAAGAAGACATTTGCCGCAACCAAGAGCTGTGATGAGTCACTGA 2603
QY 556 CGGATTTGCCAATACAGTGGCAGTTGGGAAGATGAGCAGTTGTTATGACCAATT 615
DB 2604 CGGATTTGCCAATACAGTGGCAGTTGGGAAGATGAGCAGTTGTTATGACCAATT 2663
QY 616 TAAATAAAGACGTCAGGAATTGACTGATCAAAATTGCAACAGAGTTGGTGTAGACT 675
DB 2664 TAAATAAAGACGTCAGGAATTGACTGATCAAAATTGCAACAGAGTTGGTGTAGACT 2723
QY 676 CAACCTGTACCTAAACGAATTGACTGATCAATTGCAACCAATCACTTCACTGCTTT 735
DB 2724 CAACCTGTACCTAAACGAATTGACTGATCAATTGCAACCAATCACTTCACTGCTTT 2783
QY 736 AAACAAGCTACATTTAGGCACTTTCATCTGAGTGGGGAATATGATTTACTTATT 795
DB 2784 AAACAAGCTACATTTAGGCACTTTCATCTGAGTGGGGAATATGATTTACTTATT 2843
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DB 2844 GACTAAGTATGATGAGGAACAATCAATCACTGATCTTAACTCGGTAGCGGCTTAATCAC 2903
QY 856 CGGTAAACCTATTTCTATACGATCAACAGACTCAACTCTGGGGTATACAGTAACTTACC 915
DB 2904 CGGTAAACCTATTTCTATACGATCAACAGACTCAACTCTGGGGTATACAGTAACTTACC 2963
QY 916 TTTCAGTGGGAACCTAATAATATGCGTGGCACTTCTGGAACCTTAATCCGTAACAC 975
DB 2964 TTTCAGTGGGAACCTAATAATATGCGTGGCACTTCTGGAACCTTAATCCGTAACAC 3023
QY 976 AACCAAGGATTTGCTCGGCACTTGTCCCAAAAGGTGTGACACAGGTCGGTTCTGTGAT 1035
DB 3024 AACCAAGGATTTGCTCGGCACTTGTCCCAAAAGGTGTGACACAGGTCGGTTCTGTGAT 3083
QY 1036 AGAAGAACTTGACACCTCATATGTTATAGAAAGTGAAGTTTATATTTGTACAGAAAT 1095
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DB 3084 AGAAGAACTTGACACCTCATATGTTATAGAAAGTGAAGTTTATATTTGTACAGAAAT 3143
QY 1096 AGTAACCTTCCATATGTCCTCGGTATTTATTTCTGCTTGAAGCGGCAATACGTCGCTG 1155
DB 3144 AGTAACCTTCCATATGTCCTCGGTATTTATTTCTGCTTGAAGCGGCAATACGTCGCTG 3203
QY 1156 TATGATCTCAAAAGCCGAAGCGGCACTTATACACCTATACATGATCTATCAAAGTTACGT 1215
DB 3204 TATGATCTCAAAAGCCGAAGCGGCACTTATACACCTATATATGATCTATCAAAGCTTACGT 3263
QY 1216 CATGCGCAATGCAAGATGACCAATGATGATGTTAAACCCCGGGGTATCATATGCA 1275
DB 3264 CATGCGCAATGCAAGATGACCAATGATGATGTTAAACCCCGGGGTATCATATGCA 3323
QY 1276 AAATATAGGAAGCCGTGCTCTAATATGATTAACAATCATATGCAATGTTATCTTACG 1335
DB 3324 AAATATAGGAAGCCGTGCTCTAATATGATTAACAATCATATGCAATGTTATCTTACG 3383
QY 1336 CGGGATTAACCTTTAAGGCTCACTGGGGAAATTCGATGTAACCTTATCAAGAAATATCTCAAT 1395
DB 3384 CGGGATTAACCTTTAAGGCTCACTGGGGAAATTCGATGTAACCTTATCAAGAAATATCTCAAT 3443
QY 1396 ACAAGATTCACAGTATATATACAGGCAATCTTATATCTCAATGATGAGCTGGGAATGT 1455
DB 3444 ACAAGATTCACAGTATATATACAGGCAATCTTATATCTCAATGATGAGCTGGGAATGT 3503
QY 1456 CAACAATCTGATCAGTAATGCTTTGATTAAGATTAAGAGAAAGCAACAGAAACCTAGACAA 1515
DB 3504 CAACAATCTGATCAGTAATGCTTTGATTAAGATTAAGAGAAAGCAACAGAAACCTAGACAA 3563
QY 1516 AGTCAATGTCAAACTGACTGACATCTGCTCTCATATTAAGATTAATGCTTTGACTATCAT 1575
DB 3564 AGTCAATGTCAAACTGACTGACATCTGCTCTCATATTAAGATTAATGCTTTGACTATCAT 3623
QY 1576 ATCTGTTGTTTGGTATTAATCTTATGAGCTGATTTAGACATGCTACTAATGTACAAAGCAAAA 1635
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QY 1636 GGGGCAACAAAAAACTTATATGCTTTGGAAATATATCTTATGATCAGATGAGAGCCAC 1695
DB 3684 GGGGCAACAAAAAACTTATATGCTTTGGAAATATATCTTATGATCAGATGAGAGCCAC 3743
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DB 3744 TACAAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATATGTAATTTGTGAAG 3803
QY 1756 TTCTGTAGTCTGTCAAGTTCAGAGATTAAGAAAAA 1792
DB 3804 TTCTGTAGTCTGTCAAGTTCAGAGATTAAGAAAAA 3840

RESULT 14
ABK30556
ID ABK30556 standard; cDNA; 3570 BP.
XX
AC ABK30556;
XX
DT 15-NOV-2002 (first entry)
XX
DE Newcastle disease virus (NDV) fusion gene.
XX
KW Newcastle disease virus; gene; ss; novel recombinant avian herpesvirus;
XX NAHV; herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
XX infectious laryngotracheitis; virucide; immunostimulant; vaccine; NDV.
XX
OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT CDS 1194..2888
FT /feature = a
FT /product = "Newcastle disease virus protein"
FT /transl_except = (pos:1353..1355, aa:Xaa)
```

FT /note= "Xaa= unknown"  
 XX US2002081316-A1.  
 XX 27-JUN-2002.  
 XX 14-JUN-2001; 2001US-00881457.  
 XX 12-JUN-1992; 92US-00898087.  
 PR 26-FEB-1993; 93US-00023610.  
 PR 14-JUN-1993; 93WO-US005681.  
 PR 09-AUG-1994; 94US-00288055.  
 PR 13-JUN-1995; 95WO-US010245.  
 PR 21-FEB-1997; 96US-00663566.  
 PR 25-OCT-1999; 97US-00804372.  
 PR 99US-00426352.  
 XX (COCH/) COCHRAN M D.  
 PA (COOK/) COOK S M.  
 PA (WILD/) WILD M A.  
 PI Cochran MD, Cook SM, Wild MA;  
 XX WPI; 2002-635456/68.  
 DR P-PSDB; ABG31709.  
 XX Novel recombinant avian herpesvirus comprising unique long and repeat  
 PT genome regions of herpes virus of turkeys, unique short viral  
 PT genome region of Marek's disease virus, and optional foreign DNA  
 PT sequence.  
 XX Disclosure; Page 12-14; 26pp; English.  
 PS The invention relates to a novel recombinant avian herpesvirus (NAHV)  
 CC comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat  
 CC genome region and a Marek's disease virus unique short (US) viral  
 CC genome region where at least one foreign DNA sequence is inserted within  
 CC a US2 gene of the US region of the NAHV, and is capable of being  
 CC expressed in a host cell. NAHV is useful for producing vaccines used for  
 CC immunizing an avian species against Newcastle disease, infectious  
 CC laryngotracheitis and Marek's disease. This sequence represents a  
 CC Newcastle disease virus (NDV) fusion gene  
 CC XX  
 SQ Sequence 3570 BP; 982 A; 857 C; 845 G; 885 T; 0 U; 1 Other;  
 Query Match 50.7%; Score 1701.6; DB 6; Length 3570;  
 Best Local Similarity 98.4%; Pred. No. 0;  
 Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;  
 QY 16 TGAATCCCGGTTGGGCGCCCTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75  
 Db 1199 TCGATCCCGGTTGGGCGCCCTCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 1258  
 QY 76 AGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGATGTCATCTGTCGGCAAA 135  
 Db 1259 AGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGATGTCATCTGTCGGCAAA 1318  
 QY 136 CTCATTGATGAGGAGGCTCTTTGAGCTGCAAGAAATTGTGTTACAGAGACAAAGCCGT 195  
 Db 1319 CTCATTGATGAGGAGGCTCTTTGAGCTGCAAGG-ACITGTTTACAGAGACAAAGCAAT 1377  
 QY 196 CAACATATACACTCATCCAGACAGATGATCATATGTTAAGCTCTCCGAATCTGCC 255  
 Db 1378 CAACATATACACTCATCCAGACAGG-TCAATCTTA-TTAAGCTCTCCGAATCTGCC 1435  
 QY 256 CAAGATTAAGAGGAGGATGCGAAAGCCCTTGATGATCAACAGAGCAATTGACAC 315  
 Db 1436 AAAGATTAAGAGGAGGATGCGAAAGCCCTTGATGATCAACAGAGCAATTGACAC 1495  
 QY 316 TTTTCTACCCCCCTTGGTGACTCTATCCGTAAGATTAAGAGTGTGATCACTACCTGG 375  
 Db 1496 TTTTCTACCCCCCTTGGTGACTCTATCCGTAAGATTAAGAGTGTGATCACTACCTGG 1555

QY 376 AGGGGGGAGACAGGGGCGCCCTTATAGGCGCATTAATTTGGCGGTGCTCTTGGGTTGC 435  
 Db 1556 AGGGGGGAGACAGGGGCGCCCTTATAGGCGCATTAATTTGGCGGTGCTCTTGGGTTGC 1615  
 QY 436 AACTGCGGACAAATTAACAGGGGCGGAGCTCTGATACAGAGCAAAATGCTGCCAA 495  
 Db 1616 AACTGCGGACAAATTAACAGGGGCGGAGCTCTGATACAGAGCAAAATGCTGCCAA 1675  
 QY 496 CATCTCCGACTTAAGAGAGCATTTGCCCAACCAATGAGGCTGTGATGAGCTGA 555  
 Db 1676 CATCTCCGACTTAAGAGAGCATTTGCCCAACCAATGAGGCTGTGATGAGCTGA 1735  
 QY 556 CGGATTTACGAATCAGAGTGGCACTTTGGGAAGATGACAGATTTGTTATGACCAAT 615  
 Db 1736 CGGATTTACGAATCAGAGTGGCACTTTGGGAAGATGACAGATTTGTTATGACCAAT 1795  
 QY 616 TAAATTAACAGCTAGGAAATTAAGCTGATCAAAATTTGCAAGCAAGTTGGTATGAGCT 675  
 Db 1796 TAAATTAACAGCTAGGAAATTAAGCTGATCAAAATTTGCAAGCAAGTTGGTATGAGCT 1855  
 QY 676 CAACCTGACCTTAACCGAATTTGACTACAGTATTTGCAACCAATCACTTCACTGCTTT 735  
 Db 1856 CAACCTGACCTTAACCGAATTTGACTACAGTATTTGCAACCAATCACTTCACTGCTTT 1915  
 QY 736 AAACAGCTGACTATTCAGGCACTTTACATCTAGCTGTGGAAATATGATTTACTTAT 795  
 Db 1916 AAACAGCTGACTATTCAGGCACTTTACATCTAGCTGTGGAAATATGATTTACTTAT 1975  
 QY 796 GACTAAGTTAGGTATGAGGAACATCACTAGGCTATTAATTCGGTAGCGGCTTAATAC 855  
 Db 1976 GACTAAGTTAGGTATGAGGAACATCACTAGGCTATTAATTCGGTAGCGGCTTAATAC 2035  
 QY 856 CGGTAAACCTTATCTATACGACTCAAGACTCAACTCTTGGGTATACAGTAACTCTAC 915  
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 QY 916 TTCACTGCGGAACCTAAATTAATATGCGTCCACCTACTTGGAAACCTTATCCGTAGAC 975  
 Db 2096 TTCACTGCGGAACCTAAATTAATATGCGTCCACCTACTTGGAAACCTTATCCGTAGAC 2155  
 QY 976 AAACAGGGGATTTGCTCCGCACTTGTCCCAAAAGTGTGACAGAGTCGGTTCGTAT 1035  
 Db 2156 AAACAGGGGATTTGCTCCGCACTTGTCCCAAAAGTGTGACAGAGTCGGTTCGTAT 2215  
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 Db 2216 AGAAGACTTGAACACTGATCTGATATGAAGAACTGATTAATTTATTTGATCAAGAT 2275  
 QY 1156 TATGTACTCAAAAGCCGAAGGCGCACTTATCAACATATGACTATCAAAAGTTCACT 1215  
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 QY 1276 AAATATGAGAGACCGGTCTCTAATATGATTAACATCATGCAATGTTTATCTTAAG 1335  
 Db 2456 AAATATGAGAGACCGGTCTCTAATATGATTAACATCATGCAATGTTTATCTTAAG 2515  
 QY 1336 CGGATTAACCTTAAGAGCTCAATGGGGAATTTGATGATTAATTTATGAGAAATATCTCAAT 1395  
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 Db 2576 ACAAGATTCTCAAGTAATTAACAGGCACTTGAATCTCAACTGAGCTTGGGAATGT 2635  
 QY 1456 CAACAACTCGATCAGTAATGCTTTGAATTAAGTGAAGAAAGCAACAGAAATCTAGCAA 1515

Db	2636	CACACACTCGATCAGTAATGCCCTTGAAATTAAGTAGAGAAAAGCAACGAAAACCTAGACA	2635
Qy	1516	AGTCAATGTCAAACTGACTAGACATCTGCTCTCATTAACCTATATCGTTTGACTATCAT	1515
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Db	2756	ATCTCTGTTTTTGGTATACCTTAGCCGTAATCTTAGACGTACCTTAAGTACAAAGCAAA	2815
Qy	1636	GGCGCAACAAAACCTTATTATGGCTTGGGAATATATCTTAGATCAGTAGAGCCAC	1695
Db	2816	GGCGCAACAAAACCTTATTATGGCTTGGGAATATATCCTTAGATCAGTAGAGCCAC	2875
Qy	1696	TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAGTAATTTGTGTAAAG	1755
Db	2876	TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAGTAATTTGTGTAAAG	2935
Qy	1756	TTCTGTGTAGTCTGTCAATTCAGAGAGTTTAAGAAAAA	1792
Db	2936	TTCTGTGTAGTCTGTCAATTCAGAGAGTTTAAGAAAAA	2972

RESULT 15	
AA18203	
ID	AA18203 standard; DNA; 1662 BP.
XX	
AC	AA18203;
XX	
DT	04-MAR-1997 (first entry)
XX	
DE	Newcastle disease virus F gene.
XX	
KW	Turkey herpes Virus; recombinant virus; vaccine; prophylaxis;
KW	immunisation; avian virus; infectious bronchitis virus;
KW	infectious bursal disease virus; Newcastle disease virus;
KW	Marek's disease virus; infectious laryngotracheitis virus; IBV; IBDV;
KW	NDV; MDV; ILV; ds.
XX	
OS	Newcastle disease virus.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..1662
FT	/*tag= a
FT	/product= "NDV F gene product"
XX	
PN	W09605291-A1.
XX	
PD	22-FEB-1996.
XX	
PF	09-AUG-1995; 95WC-US010245.
XX	
PR	09-AUG-1994; 94US-00288065.
PR	22-DEC-1994; 94US-00362240.
XX	
PA	(SYTR ) SYNTRO CORP.
XX	
PI	Cochran MD, Junker DE, Wild MA, Singer PA;
XX	
DR	WPI; 1996-139689/14.
DR	P-PSDB; AAM06828.
XX	
PT	Recombinant turkey herpes viruses contg. foreign DNA encoding a cytokine
PT	- useful in vaccines to protect against Marek's disease virus and other
PT	avian viruses.
XX	
PS	Disclosure; Page 177-179; 249pp; English.
XX	
CC	Recombinant turkey herpes virus (rTH) which comprise a foreign DNA
CC	sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9
CC	genomic fragment, where the cytokine can be expressed in host cells
CC	infected with the virus can be used in vaccines to protect turkeys

CC	against avian viruses. The recombinant viruses can be used for immunising
CC	birds against infectious bronchitis virus (IBV), infectious bursal
CC	disease virus (IBDV), Marek's disease virus (MDV), infectious
CC	laryngotracheitis virus (ILV) and Newcastle disease virus (NDV). They may
CC	also be used in multivalent vaccines to protect against two or more of
CC	these avian viruses. This sequence is the F gene of the Newcastle disease
CC	virus and encodes an antigen which can be used in the recombinant
CC	vaccines
SQ	Sequence 1662 BP; 507 A; 390 C; 353 G; 412 T; 0 U; 0 Other;
XX	
Query Match	48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity	98.9%; Pred. No. 0; Mismatches 19; Indels 0; Gaps 0;
Matches 1643; Conservative	0; Gaps 0;
DG	47 ATGGGCTTCAGACCTTCTCACAGAACCCAGCACCCTATGTAGTCGTAATCCGGGTTGCG 106
DG	1 ATGGGCTTCACACTTCTCAACAGAACCCAGCACCCTATGTAGTCGTAATCCGGGTTGCG 60
DG	107 CTGGCACTAGTTGCATCTGTCCGGCAAACCTCCATTGATGGCAGGCTCTTGCACTGCCA 166
DG	61 CTGGTACTGAATGCATCTGTCCGGCAAACCTCCATTGATGGCAGGCTCTTGCACTGCCA 120
DG	167 GGAAATTGGTTTACAGAGACAAGAACCCTGAACATATACCTCATCCCAACAGATCA 226
DG	121 GGAAATTGGTTTACAGAGACAAGAACCCTGAACATATACCTCATCCCAACAGATCA 180
DG	227 ATCATAGTTAAGCTCTCCCGAATCTGCCCCAAGATAAGAGAGCATGNCAGAAACCCC 286
DG	181 ATCATAGTTAAGCTCTCCCGAATCTGCCCCAAGATAAGAGAGCATGNCAGAAACCCC 240
DG	287 TTGATGACATACCAAGGACATTGACCATTTGCTCACCCCCCTTGGTGTGACTATCCGT 346
DG	241 TTGATGACATACCAAGGACATTGACCATTTGCTCACCCCCCTTGGTGTGACTATCCGT 300
DG	347 AGGATACAGAGTCTGTGATCTCAATCTTGAGAGGGGGGAGACAGGGGGCCCTTATAGGCGC 406
DG	301 AGGATACAGAGTCTGTGATCTCAATCTTGAGAGGGGGGAGACAGGGGGCCCTTATAGGCGC 360
DG	407 ATTATGGCGGTGTGGCTCTTGGGGATTGCCAATCCCGCAAAATPACAGCGGCGCAGCT 466
DG	361 ATTATGGCGGTGTGGCTCTTGGGGATTGCCAATCCCGCAAAATPACAGCGGCGCAGCT 420
DG	467 CTGATACAGGCCAAACAAAATGTCGCCAATCTCCGACTTAAAGAGAGCATTTGCCGA 526
DG	421 CTGATACAGGCCAAACAAAATGTCGCCAATCTCCGACTTAAAGAGAGCATTTGCCGA 480
DG	527 ACCAATGAGGCTGTGCATGAGGTCACTGACCGAATTAATCCGAATNAGAGTGGCAGTTGG 586
DG	481 ACCAATGAGGCTGTGCATGAGGTCACTGACCGAATTAATCCGAATNAGAGTGGCAGTTGG 540
DG	587 AAGATGCAAGCTTGTGTTAATGACCAATTTAATAAAAACAGCTCAGAAATTAGCTGATC 646
DG	541 AAGATGCAAGCTTGTGTTAATGACCAATTTAATAAAAACAGCTCAGAAATTAGCTGATC 600
DG	647 AAAATTGCAAGCAAGTTGTGTGAGGTCACTGACCTTAACAGCATTAATGACTACAGTA 706
DG	601 AAAATTGCAAGCAAGTTGTGTGAGGTCACTGACCTTAACAGCATTAATGACTACAGTA 660
DG	707 TTGGGACCAAAATCACTTCACTGCTGTGTTTTAACAAGCTGACTATTTACAGCACTTTACAAT 766
DG	661 TTGGGACCAAAATCACTTCACTGCTGTGTTTTAACAAGCTGACTATTTACAGCACTTTACAAT 720
DG	767 CTAGCTGTGTAATAATGAGATTACTTTATGCTAATGAGTTAGGTTAGGAACAATCAATC 826
DG	721 CTAGCTGTGTAATAATGAGATTACTTTATGCTAATGAGTTAGGTTAGGAACAATCAATC 780
DG	827 AGCTCATTAATCGGTAGCGGCTTATATACACCGGTAACCTTATCTATACATCAGACT 886
DG	781 AGCTCATTAATCGGTAGCGGCTTATATACACCGGTAACCTTATCTATACATCAGACT 840
DG	887 CAACCTTTGGGTATACAGGTAACTCTACCTTCACTGGGAACTTAATATATGCGTGGC 946



Db 841 CAACCTTTGGGTATACAGGTAACTTACCTTCAGTCGGGAACTTAATATATGCGTCC 900  
Qy 947 ACCTACTTGGAAACCTTATCCGTAAAGCAAAACAGGGGATTTGCTCGGCACTTGCCCA 1006  
Db 901 ACCTACTTGGAAACCTTATCCGTAAAGCAAAACAGGGGATTTGCTCGGCACTTGCCCA 960  
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Db 961 AAAGTGTGACACGGGTGCGTTCGTGTATAGAAAGAACTTGAACCTCATCTGTATAGAA 1020  
Qy 1067 ACTGACTTGAATTTATTTATTTAGCAAGATAGTAAAGTCCCTATGTCCCGTGTATTTAT 1126  
Db 1021 ACTGACTTGAATTTATTTATTTAGCAAGATAGTAAAGTCCCTATGTCCCGTGTATTTAC 1080  
Qy 1127 TCCTGCTTGAGCGGCAATAGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACT 1186  
Db 1081 TCCTGCTTGAGCGGCAATAGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACT 1140  
Qy 1187 ACACCATATCATGACTATCAAAAGTTCACTCATCGGCAACTGCAAGATGACAAACATGTAGA 1246  
Db 1141 ACACCATATATGACTATCAAAAGCTCAGTCATCGCTAACCTGCAAGATGACAAACATGTAGA 1200  
Qy 1247 TGTGTAAACCCCGGGGTATCATATCGCAAAACTATGGAGAACCGGTCTCTAATAGAT 1306  
Db 1201 TGTGTAAACCCCGGGGTATCATATCGCAAAACTATGGAGAACCGGTCTCTAATAGAT 1260  
Qy 1307 AACCAATCATCAATGTTTATCTTATCGTGGGGAATTAATTAAAGGCTCAGTGGGAATTC 1366  
Db 1261 AACCAATCATCAATGTTTATCTTATCGTGGGGAATTAATTAAAGGCTCAGTGGGAATTC 1320  
Qy 1367 GATGTAACTTATCAGAAAGATATCTCAATACAAAGTTCTCAAGTAAATATTAACAAGGCAAT 1426  
Db 1321 GATGTAACTTATCAGAAAGATATCTCAATACAAAGTTCTCAAGTAAATATTAACAAGGCAAT 1380  
Qy 1427 CTTGATATCTCACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATAAG 1486  
Db 1381 CTTGATATCTCACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAATAAG 1440  
Qy 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCT 1546  
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Qy 1607 CTAGCATGCTTACCTTATGTACAGCAAAAGCGCAACAAAACCTTATTTATGCTTGGG 1666  
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Db 1621 AATAATCTCTAGATCAGATGAGAGCCACTAACAAAATGTGA 1662

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Job time : 1908 secs

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OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 21:39:14 ; Search time 569 Seconds  
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10490.425 Million cell updates/sec

Title: US-10-800-256-1

Perfect score: 3358  
Sequence: 1 acgggtgagaagattctggat.....cctaactctatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3353.2	99.9	15186	3	US-09-741-744A-134
2	3196.4	95.2	3825	9	US-06-781-510678
3	1741.8	51.9	4177	2	US-08-484-575A-12
4	1741.8	51.9	4177	3	US-08-477-459-12
5	1741.8	51.9	4177	3	US-08-479-869-12
6	1741.8	51.9	4177	3	US-08-486-414-12
7	1741.8	51.9	4177	6	PCT-US94-01826A-12
8	1741.8	51.9	4177	6	PCT-US94-02522A-12
9	1701.6	50.7	3570	3	US-09-881-457A-1
10	1631.6	48.6	1662	2	US-08-663-566A-12
11	1631.6	48.6	1662	2	US-08-023-610-12
12	1631.6	48.6	1662	2	US-08-288-065A-12
13	1631.6	48.6	1662	2	US-08-362-240A-12
14	1631.6	48.6	1662	2	US-08-804-372A-10
15	1631.6	48.6	1662	6	PCT-US95-10245-12
16	1511	45.0	1907	2	US-07-820-154A-29
17	1511	45.0	1907	2	US-08-097-554A-29
18	1511	45.0	1907	3	US-08-480-640A-29
19	1511	45.0	1907	3	US-08-295-802-29
20	1511	45.0	1907	3	US-08-488-237A-29
21	1511	45.0	1907	3	US-08-375-992A-29
22	1511	45.0	1907	3	US-08-472-679H-29
23	1511	45.0	1907	6	PCT-US93-00324-29
24	1448	43.1	2176	2	US-07-778-890A-2

25	1421.6	42.3	1734	2	US-08-663-566A-10	Sequence 10, Appl
26	1421.6	42.3	1734	2	US-08-023-610-10	Sequence 10, Appl
27	1421.6	42.3	1734	2	US-08-288-065A-10	Sequence 10, Appl
28	1421.6	42.3	1734	2	US-08-362-240A-10	Sequence 8, Appl1
29	1421.6	42.3	1734	2	US-08-804-372A-8	Sequence 10, Appl1
30	1421.6	42.3	1734	6	PCT-US95-10245-10	Sequence 10, Appl1
31	1414	42.1	1662	3	US-10-725-841-1	Sequence 16, Appl
32	1368.4	40.8	2521	2	US-08-368-803-16	Sequence 18, Appl
33	1368.4	40.8	2521	2	US-08-578-096A-18	Sequence 8, Appl1
34	1368.4	40.8	2521	3	US-08-790-517-8	Sequence 18, Appl
35	1368.4	40.8	2521	3	US-09-240-426-18	Sequence 18, Appl
36	1368.4	40.8	2521	3	US-09-219-932-14	Sequence 10, Appl
37	1368.4	40.8	2521	3	US-09-362-831-8	Sequence 8, Appl1
38	1362.8	40.6	1662	3	US-09-232-479-10	Sequence 10, Appl
39	1362.8	40.6	1662	3	US-09-784-990-10	Sequence 10, Appl
40	1160.8	34.6	1716	3	US-09-232-479-7	Sequence 7, Appl1
41	1160.8	34.6	1716	3	US-09-784-990-7	Sequence 7, Appl1
42	127.2	3.8	1685	2	US-08-105-483-370	Sequence 370, App
43	127.2	3.8	1685	2	US-08-709-209-370	Sequence 370, App
44	127.2	3.8	1685	2	US-08-458-101-370	Sequence 370, App
45	120.2	3.6	1656	2	US-08-700-548-3	Sequence 3, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-741-744A-134  
Sequence 134, Application US/09741744A  
Patent No. 6719979  
GENERAL INFORMATION:  
APPLICANT: Peeters, Bernadus  
APPLICANT: de Leeuw, Olav  
APPLICANT: Klaus, Guus  
APPLICANT: Arroud, Ghelens  
TITLE OR INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic  
FILE REFERENCE: 2183-4646US  
CURRENT FILING DATE: 2000-12-19  
PCT APPLICATION NUMBER: 2000-12-19  
PRIOR FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 134  
LENGTH: 15186  
TYPE: DNA  
ORGANISM: Newcastle disease virus LaSota  
US-09-741-744A-134

Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ACGGGTGAGAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
DB	4498	ACGGGTGAGAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
QY	61	TTTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTGGCGCTGACCTGAGTTG	120
DB	4558	TTTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTGGCGCTGACCTGAGTTG	4617
QY	121	CATCTGTCGGCAACTCATTTGATGAGAGGCTCTTGCAGCTGCAGGAATTGGTTAC	180
DB	4618	CATCTGTCGGCAACTCATTTGATGAGAGGCTCTTGCAGCTGCAGGAATTGGTTAC	4677
QY	181	AGGAGACAAAGCCGTCAATATACCTATATCCCAAGAGATCAATGATTAAGT	240
DB	4678	AGGAGACAAAGCCGTCAATATACCTATATCCCAAGAGATCAATGATTAAGT	4737
QY	241	CTCTCCGATCTGCGCAAGTAAGAGGAGGATGTCGCAAGCCCTCTTGATGATACAA	300
DB	4738	CTCTCCGATCTGCGCAAGTAAGAGGAGGATGTCGCAAGCCCTCTTGATGATACAA	4797

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Db 4798 CAGGACATTGACCACTTTCCTCACACCCCTTGGTGACTCTATCCGTAAGATTACAAGATC 4857  
QY 361 TGTGACATCAATCTGAGAGGGGGAGACAGGGGCGCTTATATAGCGCCATTATTTGGCGGTG 420  
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QY 421 GGCTCTTGGGGTGGCAACCTGCGGCAAAATACAGCGGCGGAGCTGTGATACAGCCAA 480  
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Db 5038 GCATGAGGTCACTGACCGGATTATCGCAACTGACGTGGCAGTTGGGAGAGATGACAGAGTT 5097  
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QY 1321 TGTATTAATCTTATGGGGGGAATCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380  
Db 5818 TGTATTAATCTTATGGGGGGAATCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877  
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Db 5878 GAAGAAATATCTCAATACAAAGATTTCTCAAGTATATTAATAACAGGCAATCTTGTATCTCAAC 5937  
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QY 1501 CAGAAAATCTAGCAAAAGTCAATGTCAAACTGACTAGACACATCTGCTCTCATTAACCTTAT 1560  
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QY 1561 CGTTTGAATCAATATCTGTTTGGTATCTTACGCTGATTTAGCATCTACT 1620  
Db 6058 CGTTTGAATCAATATCTGTTTGGTATCTTACGCTGATTTAGCATCTACT 6117  
QY 1621 AATGTACAAAGCAAAAGCGCAACAAAACCTTATTAATGCTTGGAAATTAATCTTGA 1680  
Db 6118 AATGTACAAAGCAAAAGCGCAACAAAACCTTATTAATGCTTGGAAATTAATCTTGA 6177  
QY 1681 TCAGATGAGACCACTTCAAAAATGTGAACAAGATGAGAACAGAGTTTCCCTAATAG 1740  
Db 6178 TCAGATGAGACCACTTCAAAAATGTGAACAAGATGAGAACAGAGTTTCCCTAATAG 6237  
QY 1741 TAAATTTGTGAAAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAACCTAACGGT 1800  
Db 6238 TAAATTTGTGAAAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAACCTAACGGT 6297  
QY 1801 TGTATATGACCAAAAGACGATATACGGGTAGAAACGTTAAGAGAGCCGCCCTCAATTTGC 1860  
Db 6298 TGTATATGACCAAAAGACGATATACGGGTAGAAACGTTAAGAGAGCCGCCCTCAATTTGC 6357  
QY 1861 GAGCAAGGCTTCAACAACCTCCGTTCTACCGCTTCAACGACAACAGTCTCAATCATGAC 1920  
Db 6358 GAGCAAGGCTTCAACAACCTCCGTTCTACCGCTTCAACGACAACAGTCTCAATCATGAC 6417  
QY 1921 CGGCGGCTTATAGCCAGTTGGGTTATAGAAATGATGAAAAGAACCAAAATATACATGCGC 1980  
Db 6418 CGGCGGCTTATAGCCAGTTGGGTTATAGAAATGATGAAAAGAACCAAAATATACATGCGC 6477  
QY 1981 TTGATATTCGGAATGGAATCTTATTTCTTAACAGTATGACCTTGGCTATATCTGTAGCC 2040  
Db 6478 TTGATATTCGGAATGGAATCTTATTTCTTAACAGTATGACCTTGGCTATATCTGTAGCC 6537  
QY 2041 TCCCTTTATATATGACATGAGGAGCTAGACACCTAGCGATCTTGTAGCATACCGACTAGG 2100  
Db 6538 TCCCTTTATATATGACATGAGGAGCTAGACACCTAGCGATCTTGTGTAGCATACCGACTAGG 6597  
QY 2101 ATTTCCAGGCGAAGAAAAGATTACATCTTACCTTGTCCATCAAGATGTATGAT 2160  
Db 6598 ATTTCCAGGCGAAGAAAAGATTACATCTTACCTTGTCCATCAAGATGTATGAT 6657  
QY 2161 AGGATATATTAAGCAAGTGGGCTTGAATCTCCGTTGACATTTGTTAAATCTAGAACACA 2220  
Db 6658 AGGATATATTAAGCAAGTGGGCTTGAATCTCCGTTGACATTTGTTAAATCTAGAACACA 6717  
QY 2221 ATTATGAACGCAATTAACATCTCTCTTATCAGATTAAATGAGCTGCAACCAAGTGG 2280  
Db 6718 ATTATGAACGCAATTAACATCTCTCTTATCAGATTAAATGAGCTGCAACCAAGTGG 6777  
QY 2281 TGGGGGCGACTTATCCATGACCAAGTATATAGGGGGATAGGCAAAAGACTATTTGTA 2340  
Db 6778 TGGGGGCGACTTATCCATGACCAAGTATATAGGGGGATAGGCAAAAGACTATTTGTA 6837  
QY 2341 GATGATGCTATGATGACATGATCTATCCCTGCAATTTGAAGAACTGGAATTTT 2400  
Db 6838 GATGATGCTATGATGACATGATCTATCCCTGCAATTTGAAGAACTGGAATTTT 6897  
QY 2401 ATCCCGGCGCTTACTACAGGATCAGGTGCACTCGAATACCTCATTTGACATGAGTGT 2460  
Db 6898 ATCCCGGCGCTTACTACAGGATCAGGTGCACTCGAATACCTCATTTGACATGAGTGT 6957  
QY 2461 ACCCATTAATGCTACACCAATTAATGTATATTTGTCTGATGACAGAGATCTCAATTTCA 2520

Db 6958 ACCATTACTGCTACACCCATATATATATGCTGATGACAGATCACTCAATTCA 7017  
Qy 2521 TATCAGATTATTAGACATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Db 7018 TATCAGATTATTAGACATTTGGTGTCTCCGACATCTGCAACAGGAGGATTTCTTTCT 7077  
Qy 2581 ACTCTGCTTTCATCAACCTTGGACGACACCCAAATGGAAGTCTTGACGTGTAGTCCA 2640  
Db 7078 ACTCTGCTTTCATCAACCTTGGACGACACCCAAATGGAAGTCTTGACGTGTAGTCCA 7137  
Qy 2641 ACTCCCTGGGTGTGTATGATGCTGTGCTCGAAGTCAACGAGACAGAGGAAGATTAT 2700  
Db 7138 ACTCCCTGGGTGTGTATGATGCTGTGCTCGAAGTCAACGAGACAGAGGAAGATTAT 7197  
Qy 2701 AACTCAGCTGTCTCTAGCGGATGTATCATGAGAGTTAGGGTTGACGCGCAGTACAC 2760  
Db 7198 AACTCAGCTGTCTCTAGCGGATGTATCATGAGAGTTAGGGTTGACGCGCAGTACAC 7257  
Qy 2761 GAAAAGACCTAGATGTCACAACTTATTCGGGGACTGGGTGGCCAACTACCCAGAGTA 2820  
Db 7258 GAAAAGACCTAGATGTCACAACTTATTCGGGGACTGGGTGGCCAACTACCCAGAGTA 7317  
Qy 2821 GGGGGTGGATCTTTTATTTGAAGCGGATGATGTTCTCAGTCTACGAGGGTTAAACCC 2880  
Db 7318 GGGGGTGGATCTTTTATTTGAAGCGGATGATGTTCTCAGTCTACGAGGGTTAAACCC 7377  
Qy 2881 AATTCAACCAAGTGAACCTGTACAGAAAGGAAATATGATATACAAAGCAGTACATGAC 2940  
Db 7378 AATTCAACCAAGTGAACCTGTACAGAAAGGAAATATGATATACAAAGCAGTACATGAC 7437  
Qy 2941 ACATGCCCAATGACAAAGATACCAATTTGAAATGCAAGTCTTGATTAAGCTTGA 3000  
Db 7438 ACATGCCCAATGACAAAGATACCAATTTGAAATGCAAGTCTTGATTAAGCTTGA 7497  
Qy 3001 CGGTTTGGTGGAAACGCTATACAGAGCTATCTTATCTATCAAGGTCTCAACTCTTA 3060  
Db 7498 CGGTTTGGTGGAAACGCTATACAGAGCTATCTTATCTATCAAGGTCTCAACTCTTA 7557  
Qy 3061 GGGGAAACCGGATGATGATGATCGGCGCAACAGTCACTCATGAGGGCGGAAAGC 3120  
Db 7558 GGGGAAACCGGATGATGATGATCGGCGCAACAGTCACTCATGAGGGCGGAAAGC 7617  
Qy 3121 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCACTTCTCT 3180  
Db 7618 AGAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCACTTCTCT 7677  
Qy 3181 CCGCGTTATTATATCTATGACAGTCAAGCAAAACAGCCACTTTCATAGTCTTAT 3240  
Db 7678 CCGCGTTATTATATCTATGACAGTCAAGCAAAACAGCCACTTTCATAGTCTTAT 7737  
Qy 3241 ACATTCAATGCTTCATCTCGGCGCAGTAGTATCCCTTGCGAGGCTTCGCAAGATGCC 3300  
Db 7738 ACATTCAATGCTTCATCTCGGCGCAGTAGTATCCCTTGCGAGGCTTCGCAAGATGCC 7797  
Qy 3301 AACTGATGTATCTGAGTCTATACAGATCCATATCCCTAATCTTATATGAAC 3358  
Db 7798 AACTGATGTATCTGAGTCTATACAGATCCATATCCCTAATCTTATATGAAC 7855

RESULT 2  
5310678-2  
APPLICANT: Bingham, Richard W.; Chambers, Philip; Emmerston, Peter  
T. Millar, Neil S.  
TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES  
NUMBER OF SEQUENCES: 3  
CURRENT APPLICATION NUMBER:  
FILING DATE: 17-NOV-1989  
APPLICATION NUMBER: US/07/438, 945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 885, 765  
FILING DATE: 15-JUL-1986  
SEQ ID NO:2:

5310678-2  
LENGTH: 3825  
Query Match 95.2%; Score 3196.4; DB 9; Length 3825;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;  
Qy 1 ACGGTTGAAGATTTCTGATTCCTGGTGGGCGCTCCAGGTGCAAGATGGGCTCAAGC 60  
Db 1 ACGGTTGAAGATTTCTGATTCCTGGTGGGCGCTTCAGGTGCAAGATGGGCTCAAGC 60  
Qy 61 TTTCACAAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGACGAGTTG 120  
Db 61 TTTCACAAAGAACCCAGATCCTATGATGCTGACTATCCGGGTTGCGCTGATGAGTTG 120  
Qy 121 CATCTGCCGCAAACTCCATTGAGAGGCTCTTTCAGCTGACAGAAATTTGGTTAC 180  
Db 121 CATCTGCCGCAAACTCCATTGATGCTGACTATCCGGGTTGCGCTGACAGAAATTTGGTTAC 180  
Qy 181 AGGAGCAAAAGCGCTCAACATATACCTCATCTCCAGACAGATCATATAGTTAAGCT 240  
Db 181 AGGAGCAAAAGCGCTCAACATATACCTCATCTCCAGACAGATCATATAGTTAAGCT 240  
Qy 241 CCTCCGAATCTGCCAAGATAGAGGAGATGAGCGAAAGCCCTTGGATGATCAAA 300  
Db 241 CCTCCGAATCTGCCAAGATAGAGGAGATGAGCGAAAGCCCTTGGATGATCAAA 300  
Qy 301 CAGGACATTTGACCACTTTGCTCACCCCTTGGTGTACTATCCGTAGATACAAAGTCT 360  
Db 301 CAGGACATTTGACCACTTTGCTCACCCCTTGGTGTACTATCCGTAGATACAAAGTCT 360  
Qy 361 TGTGACTACATCTGGAGGGGAGACAGGGCGCTTATAGGCGCATTTATGGCGGTGT 420  
Db 361 TGTGACTACATCTGGAGGGGAGACAGAAACGCTTTATAGGCGCATTTATGGCGGTGT 420  
Qy 421 GGCCTTGGGTTGCACTGCGGACAAATPACAGCGCGCACTCTGATPACAGCCAA 480  
Db 421 GGCCTTGGGTTGCACTGCTGCAAAATPACAGCGCGCACTCTGATPACAGCCAA 480  
Qy 481 ACAAATGCTGCAACATCTCCGACTTAAAGAGAGATTCGCGCAACCAATGAGGCTGT 540  
Db 481 ACAAATGCTGCAACATCTCCGACTTAAAGAGAGATTCGCGCAACCAATGAGGCGGT 540  
Qy 541 GCATGAGGTCACTGACGATTTATGCAACTGACGTGCACTGAGTGGAAATGACAGCTT 600  
Db 541 GCATGAGGTCACTGACGATTTATGCAACTGACGTGCACTGAGTGGAAATGACAGCTT 600  
Qy 601 TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTTAGCTGATCAAAATTTGCACGCA 660  
Db 601 TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTTAGCTGATCAAAATTTGCACGCA 660  
Qy 661 AGTTGGTGTAGAGTCAACCTGATCACTCAACGAAATTTGCTACATTTGGAGCCAAAT 720  
Db 661 AGTTGGTGTAGAGTCAACCTGATCACTCAACGAAATTTGCTACATTTGGAGCCAAAT 720  
Qy 721 CACTTCACTGCTTTAAACAAGCTGATATTCAAGCACTTTACATCTAGCTGTGGAAA 780  
Db 721 CACTTCACTGCTTTAAACAAGCTGATATTCAAGCACTTTACATCTAGCTGTGGAAA 780  
Qy 781 TATGATTTACTTATTTGACTAATGTTAGTTAGGGAACAATTAATCACTCACTATTAATGG 840  
Db 781 TATGATTTACTTATTTGACTAATGTTAGTTAGGGAACAATTAATCACTCACTATTAATGG 840  
Qy 841 TAGGGCTTATATCACCGGTAACCTATTTATAGAGTCAAGACTCAAGCTCACTGTGGAT 900  
Db 841 TAGGGCTTATATCACCGGTAACCTATTTATAGAGTCAAGACTCAAGCTCACTGTGGAT 900  
Qy 901 ACAGTAATCTACTCTTCACTGATGAGGAACCTAATATATATGAGTCACTTATGGAAC 960  
Db 901 ACAGTAATCTACTCTTCACTGATGAGGAACCTAATATATATGAGTCACTTATGGAAC 960  
Qy 961 CTATCCGTAGAACCAACAGGGATTTGCTGCGCACTTGTCCCAAAAGTGTGACCA 1020

Db 961 CTTATCTGTAAACAACAGGGATTGCTGGCACTGTCCCAAAAAGGTGAACA 1020  
Qy 1021 GGTCGGTCTGTGTATAGAGAACTTGACACCTCATCTGTATAGAAACTGAATTG 1080  
Db 1021 GGTCGGTCTGTGTATAGAGAACTTGACACCTCATCTGTATAGAAAAGCACTTG 1080  
Qy 1081 ATATTGTACAAAGATAGTAAGTTCCCTATGTCCCTGGTATTTTATTCCTGCTGAGCG 1140  
Db 1081 ATATTGTACAAAGATAGTAAGTTCCCTATGTCCCTGGTATTTTATTCCTGCTGAGCG 1140  
Qy 1141 CAATAGCTGGCCGTGTATGTACTCAAAAGACCGAAGGGCACTTACTACCATCATGAC 1200  
Db 1141 CAATAGCTGGCCGTGTATGTACTCAAAAGACCGAAGGGCACTACTAGCCATCATGAC 1200  
Qy 1201 TATCAAGGTTCACTCATCCGCAACTGCAGATGACAAACATGTATGTATAAACCCCC 1260  
Db 1201 TATCAAGGTTCACTCATCCGCAACTGCAGATGACAAACATGTATGTATAAACCCCC 1260  
Qy 1261 GGGTATCATATCGCAAACTATGAGAAAGCCGTCTCTAATAGATTAAGCATCATGCA 1320  
Db 1261 GGGTATCATATCGCAAACTATGAGAAAGCCGTCTCTAATAGATTAAGCATCATGCA 1320  
Qy 1321 TGTTTATCCTTGGCCGGATTACTTAAAGCTCAGTGGGAAATTGATGTAACTTATCA 1380  
Db 1321 TGTTTATCCTTGGATCGGATTAAGCTTAAAGCTCAGTGGGAAATTGATGTAACTTATCA 1380  
Qy 1381 GAAGAATATCTCAATATACAAGATCTCAAGTATATTAACAGGCATCTTGATCTCAAC 1440  
Db 1381 GAAGAATATCTCAATATACAAGATCTCAAGTATATTAACAGGCATCTTGATCTCAAC 1440  
Qy 1441 TGAAGTTGGAAATGTCAACACTCGATCAGTATGCTTTGAAATGTTAAGAGAAACAA 1500  
Db 1441 TGAAGTTGGAAATGTCAACACTCGATCAGTATGCTTTGAAATGTTAAGAGAAACAA 1500  
Qy 1501 CAGAAAATCTAGCAAAAGTCAATGTCAAACTGACATGACATCTGCTCTCATTAATAT 1560  
Db 1501 CAGAAAATCTAGCAAAAGTCAATGTCAAACTGACATGACATCTGCTCTCATTAATAT 1560  
Qy 1561 CGTTTACATCATATCTCTGTGTTTGGTATGTAAGCTGATTCAGATGCTTACT 1620  
Db 1561 CGTTTACATCATATCTCTGTGTTTGGTATGTAAGCTGATTCAGATGCTTACT 1620  
Qy 1621 AATGTACAAAGCAAAAGCGCAACAAAACCTTATTAATGCTTGGAAATATATCTTGA 1680  
Db 1621 AATGTATACAAAGCAAAAGCGCAACAAAACCTTATTAATGCTTGGAAATATATCTTGA 1680  
Qy 1681 TCGATGAGAGCCCACTCAAAAATGTGAACACAGATGAGAACGAAGTTTCCCTATAG 1740  
Db 1681 TCGATGAGAGCCCACTCAAAAATGTGAACACAGATGAGAACGAAGTTTCCCTATAG 1740  
Qy 1741 TAATTTGTGAAAGTTCTGTAGTCTGTCAATTCAAGATTAAGAAAACTAACCGGT 1800  
Db 1741 TAATTTGTGAAAGTTCTGTAGTCTGTCAATTCAAGATTAAGAAAACTAACCGGT 1800  
Qy 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCCGCCCTCAATTTGC 1860  
Db 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGGTAAAGAGCCGCCCTCAATTTGC 1860  
Qy 1861 GAGCCAGGCTTCAACACTCCGTTCTACCGCTTCAACGACCAACAGTCTCATATGAGAC 1920  
Db 1861 GAGCCAGGCTTCAACACTCCGTTCTACCGCTTCAACGACCAACAGTCTCATATGAGAC 1920  
Qy 1921 CGGCGCGTTAGCAAGTTGGCTTAAGATGATGAAGAGAGGAAAAATATCATGTGCGC 1980  
Db 1921 CGGCGCGTTAGCAAGTTGGCTTAAGATGATGAAGAGAGGAAAAATATCATGTGCGC 1980  
Qy 1981 TTGATATTCGGAATTCGAATCTTATCTTAAACAGTATGACTTGGCTATATCTGTAGCC 2040  
Db 1981 TTGATATTCGGAATTCGAATCTTATCTTAAACAGTATGACTTGGCTATATCTGTAGCC 2040  
Qy 2041 TCCCTTTATATATAGATGGGGGCTAGCAACCTAGCGACTTGTAGGCATATCCGACAGG 2100  
Db 2041 TCCCTTTATATATAGATGGGGGCTAGCAACCTAGCGACTTGTAGGCATATCCGACAGG 2100

Qy 2101 ATTTCCAGGCGAAGAAAAGATTACATCTACCTTGTTCCATCAATGATGAT 2160  
Db 2101 ATTTCTTAGGCGAAGAAAAGATTACATCTGCACTTGTTCCATCAATGATGAT 2160  
Qy 2161 AGGATATATAGAAAGGCGCTTGAGTCCCGTTGGCAATTGTTAAATACATGAGACACA 2220  
Db 2161 AGGATATATAGAAAGGCGCTTGAGTCCCGTTGGCAATTGTTAAACATGAGACACA 2220  
Qy 2221 ATTAGAACGCAATTAACATCTCTCTTATCAGATTATAGAGCTGCAACACAGTGGG 2280  
Db 2221 ATTAGAACGCAATTAACATCTCTCTTATCAGATTATAGAGCTGCAACACAGTGGG 2280  
Qy 2281 TGGGGGCGACCTATCCATGACCAAGATTATAGGGGGGATAGGCAAAAGAACTCATTTGA 2340  
Db 2281 TGGGGGCGACCTATCCATGACCAAGATTATAGGGGGGATAGGCAAAAGAACTCATTTGA 2340  
Qy 2341 GATGATGCTATGATATGACATATCTATCCCTTGCAATTTCAAGAACATCTGAATTTT 2400  
Db 2341 GATGATGCTATGATATGACATATCTATCCCTTGCAATTTCAAGAACATCTGAATTTT 2400  
Qy 2401 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTCGAAATACCTCATTTGACATGAGTCT 2460  
Db 2401 ATCCCGGCGCTTACTACAGGATCAGGTTGCACTCGAAATACCTCATTTGACATGAGTCT 2460  
Qy 2461 ACCCATTAATCTGCTACACCCATTAATGTAATGTTGTGGATGACAGATCACTCAATTTCA 2520  
Db 2461 ACCCATTAATCTGCTACACCCATTAATGTAATGTTGTGGATGACAGATCACTCAATTTCA 2520  
Qy 2521 TATCAGATTTAGCATCTGGTGTGCTCCGACATCTGCAACAGGAGGGATTTCTTTCT 2580  
Db 2521 TATCAGATTTAGCATCTGGTGTGCTCCGACATCTGCAACAGGAGGGATTTCTTTCT 2580  
Qy 2581 ACTCTGGGTTGCATCAACCTGAGCAACCCAAATTCGAAAGTCTTGCACTGTGAGTGA 2640  
Db 2581 ACTCTGGGTTGCATCAACCTGAGTGTGATGACAGCCAAATTCGAAAGTCTTGCACTGTGAGTGA 2640  
Qy 2641 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAAT 2700  
Db 2641 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAAT 2700  
Qy 2701 AACTCAGCTGTCCCTTACGCGAGATGTAATGAGAGGTTAGGGTTCCAGCGCCAGTACAC 2760  
Db 2701 AACTCAGCTGTCCCTTACGCGAGATGTAATGAGAGGTTAGGGTTCCAGCGCCAGTACAC 2760  
Qy 2761 GAAAAGGACCTAGATGTCAACATTAATGGGGGACTGGGTGGCACTACCCAGAGATTA 2820  
Db 2761 GAAAAGGACCTAGATGTCAACATTAATGGGGGACTGGGTGGCACTACCCAGAGATTA 2820  
Qy 2821 GGGGGTGGATCTTTTATTTGACACCGCGTATGTTCTCACTTCAAGAGGTTAAAAACC 2880  
Db 2821 GGGGGTGGATCTTTTATTTGACACCGCGCGGTATGTTCTCACTTCAAGAGGTTAAAAACC 2880  
Qy 2881 AATTCAACCAAGTACACTGTACAGAAAGGAAATATGTGATATTAACAGCATATCATGAC 2940  
Db 2881 AATTCAACCAAGTACACTGTACAGAAAGGAAATATGTGATATTAACAGCATATCATGAC 2940  
Qy 2941 ACATGCCCAAGTACAGAACTACAGATTCGAATGGCCAAAGTCTCTGTTAAGCCCTGGA 3000  
Db 2941 ACATGCCCAAGTACAGAACTACAGATTCGAATGGCCAAAGTCTCTGTTAAGCCCTGGA 3000  
Qy 3001 CGGTTTGTGGGAAAGCATATACAGAGGCTATCTTATCTTCAAGGTTGTCAATCTTTA 3060  
Db 3001 CGGTTTGTGGGAAAGCATATACAGAGGCTATCTTATCTTCAAGGTTGTCAATCTTTA 3060  
Qy 3061 GGGGAAAGCCCGTACTGACTGTACCGCCCAACAGTCACTCATGSGGGCCGAAAGGC 3120  
Db 3061 GGGGAAAGCCCGTACTGACTGTACCGCCCAACAGTCACTCATGSGGGCCGAAAGGC 3120  
Qy 3121 AGAATTTCTCAGATAGGAGATCTCATTTTGTATCAACGAGGGTCAATATCTTCTCT 3180  
Db 3121 AGAATTTCTCAGATAGGAGATCTCATTTTGTATCAAGGAGGGTCAATATCTTCTCT 3180

QY 181 CCGCGTTATTATCTTATGACAGTCAGCAAAAGCCACTCTTTCATAGTCTTAT 3240  
DB 181 CCGCGTTATTATCTTATGACAGTCAGCAAAAGCCACTCTTTCATAGTCTTAT 3240  
QY 3241 ACATTCAATGCTTCACTCGGCGCAGGTAGTATCCCTTGCAGGCTTACAGAAAGATGCCCC 3300  
DB 3241 ACATTCAATGCTTCACTCGGCGCAGGTAGTATCCCTTGCAGGCTTACAGAAAGATGCCCC 3300  
QY 3301 AACTCGTGTACTGAGTCTATACAGATCATATCCCTTAATCTTATAGAAACC 3358  
DB 3301 AACTCGTGTACTGAGTCTATACAGATCATATCCCTTAATCTTATAGAAACC 3358

## RESULT 3

US-08-484-575A-12  
Sequence 12, Application US/08484575A  
Patent No. 5925358  
GENERAL INFORMATION:  
APPLICANT: Mark D. Cochran and David E. Junker  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,575A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq. John P  
TELEPHONE: (212)278-0450  
TELEFAX: (212)391-0525  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 115..1860  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2095..3756  
US-08-484-575A-12

Query Match 51.9%; Score 1741.8; DB 2; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTGGCGCCCTTCAGAGTGCAGATGGGCTCCAGACCTTCTACCAAGAACCC 75  
DB 2064 TCGATCCCGGTGGCGCCCTTCAGAGTGCAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123  
QY 76 AGACACCTATATGCTGACTATCCGGGTTGGCTGCGCACTGATTGCAATCTGCCGCAAA 135  
DB 2124 AGACACCTATATGCTGACTATCCGGGTTGGCTGCGCACTGATTGCAATCTGCCGCAAA 2183  
QY 136 CTCGATTGATGCGAGGCTCTTTCAGCTGCAGAAATTGTGTTTACAGAGACAAAGCCGT 195

DB 2184 CTCGATTGATGCGAGGCTCTTTCAGCTGCAGAAATTGTGTTTACAGAGACAAAGCAGT 2243  
QY 196 CAACATATACACCTCATCCCAAGACAGATCAATCATGTTAAGTCTCTCCGAATCTGCC 255  
DB 2244 CAACATATACACCTCATCCCAAGACAGATCAATCATGTTAAGTCTCTCCGAATCTGCC 2303  
QY 256 CAAGATTAAGAAAGCAATGTCGAAAGCCCTTGATGATCAATCAAGACATTTAGCAC 315  
DB 2304 AAGGATTAAGAAAGCAATGTCGAAAGCCCTTGATGATCAATCAAGACATTTAGCAC 2363  
QY 316 TTTGCTACCCCTTGTGACTCTATCCGTAGGATCAAGAGCTGTGACTACATCTGG 375  
DB 2364 TTTGCTACCCCTTGTGACTCTATCCGTAGGATCAAGAGCTGTGACTACATCTGG 2423  
QY 376 AGGGGGGAGACAGGGGCGCTTATAGGCGCATTTATGGGCTCTTGGGGTTGC 435  
DB 2424 AGGGGGGAGACAGGGGCGCTTATAGGCGCATTTATGGGCTCTTGGGGTTGC 2483  
QY 436 AACTGCCGCAAAATTAACAGCGCGCGAGCTTGTATCAAGCCCAAAATATGTCGCA 495  
DB 2484 AACTGCCGCAAAATTAACAGCGCGCGAGCTTGTATCAAGCCCAAAATATGTCGCA 2543  
QY 496 CATCTCCGACTTAAAGAGACATTGGCGCAACCAATGAGGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAAGAGACATTGGCGCAACCAATGAGGCTGTGATGAGTCACTGA 2603  
QY 556 CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATCAGCAGTTTGTAAAGCAATT 615  
DB 2604 CGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATCAGCAGTTTGTAAAGCAATT 2663  
QY 616 TAATTAACAGCTCAGGAATTTAGCTGATCAAAATTTGACAGGAAGTTGTATAGCT 675  
DB 2664 TAATTAACAGCTCAGGAATTTAGCTGATCAAAATTTGACAGGAAGTTGTATAGCT 2723  
QY 676 CAACCTGTACTTAACGGAATTGACTAGATTGCGACCAAAATCACTTCACTGCTT 735  
DB 2724 CAACCTGTACTTAACGGAATTGACTAGATTGCGACCAAAATCACTTCACTGCTT 2783  
QY 736 AAACAAGCTGACTATTCAGGCACTTTTAACTAGCTGTGGAAATATGATTAATT 795  
DB 2784 AAACAAGCTGACTATTCAGGCACTTTTAACTAGCTGTGGAAATATGATTAATT 2843  
QY 796 GACTAAGTTAGGTAGGAAACAATCACTCAGCTCAATTCGTTAGCGGCTTAATCAC 855  
DB 2844 GACTAAGTTAGGTAGGAAACAATCACTCAGCTCAATTCGTTAGCGGCTTAATCAC 2903  
QY 856 CGTTAACCTTCTATACGACTCAGACTCAACTCTTGGGTTACAGGTAATCTTACC 915  
DB 2904 CGTTAACCTTCTATACGACTCAGACTCAACTCTTGGGTTACAGGTAATCTTACC 2963  
QY 916 TTGAGTCGGGAACCTAATAATATATGCTGCGCACTTACCTTGAACCTTATCCGTAACAC 975  
DB 2964 TTGAGTCGGGAACCTAATAATATATGCTGCGCACTTACCTTGAACCTTATCCGTAACAC 3023  
QY 976 AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGTGTGACAGAGTGGTTGTGAT 1035  
DB 3024 AACCAAGGGAATTTGCTCGGCACTTGTCCCAAAAGTGTGACAGAGTGGTTGTGAT 3083  
QY 1036 AGAAGAACTTGACACCTCATATCTGTATAGAAACCTGATTTATATGTTAAGAAAT 1095  
DB 3084 AGAAGAACTTGACACCTCATATCTGTATAGAAACCTGATTTATATGTTAAGAAAT 3143  
QY 1096 AGTAAGTCCCTATGTCCTCGGTATTTATCTGTGCTTGAAGCGGCAATAGTGGGCTG 1155  
DB 3144 AGTAAGTCCCTATGTCCTCGGTATTTATCTGTGCTTGAAGCGGCAATATAGTGGGCTG 3203  
QY 1156 TATGTACTCAAGACCGAAGCGCACTTACTACCAATACATGACTATCAAGGTTCACT 1215  
DB 3204 TATGTACTCAAGACCGAAGCGCACTTACTACCAATATATGACTATCAAGGCTCAGT 3263  
QY 1216 CATGCGCAATGCGAAGTGAACAATGTAGATGTGAATCCCGGGGTTATCATATGCA 1275  
DB 3264 CATGCGCAATGCGAAGTGAACAATGTAGATGTGAATCCCGGGGTTATCATATGCA 3323



QY 1276 AAACATGAGAAAGCCGCTGCTCTAATAGATAAAACAATCATGCAATGTTTATCTTAGG 1335  
DB 3324 AAACATGAGAAAGCCGCTGCTCTAATAGATAAAACAATCATGCAATGTTTATCTTAGG 3383  
QY 1336 CGGATTAACCTTTAAGGCTCAGTGGGAAATTCAGATGAATCTTATACAGAAATATCTCAAT 1395  
DB 3384 CGGATTAACCTTTAAGGCTCAGTGGGAAATTCAGATGAATCTTATACAGAAATATCTCAAT 3443  
QY 1396 ACAAGATTCCTCAAGTAATAATAACAGCAATCTTGATATCTCAACTGAGCTGGGAATGT 1455  
DB 3444 ACAAGATTCCTCAAGTAATAATAACAGCAATCTTGATATCTCAACTGAGCTGGGAATGT 3503  
QY 1456 CAACAATCTGATCAATATGCTTGAATTAAGAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 1515  
DB 3504 CAACAATCTGATCAATATGCTTGAATTAAGAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCA 3563  
QY 1516 AGTCATATGTAACCTGACATGACATCTGCTCTCATTAATCTTATGCTTGAATCAT 1575  
DB 3564 AGTCATATGTAACCTGACATGACATCTGCTCTCATTAATCTTATGCTTGAATCAT 3623  
QY 1576 ATCTCTGTTTGGTATCTAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1635  
DB 3624 ATCTCTGTTTGGTATCTAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 3683  
QY 1636 GGGCAACCAAAAAACCTTATATGCTTGGGAATTAATCTTATGATCAGATGAGAGCCAC 1695  
DB 3684 GGGCAACCAAAAAACCTTATATGCTTGGGAATTAATCTTATGATCAGATGAGAGCCAC 3743  
QY 1696 TACAAAAATGTGAACACAGATGAGAAAGCAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 1755  
DB 3744 TACAAAAATGTGAACACAGATGAGAAAGCAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 3803  
QY 1756 TTCTGGTATCTGTCACTGATCAGAGAGTTAAGAAAAAA 1792  
DB 3804 TTCTGGTATCTGTCACTGATCAGAGAGTTAAGAAAAAA 3840

## RESULT 4

US-08-477-459-12

Sequence 12, Application US/08477459

Patent No. 6001369

GENERAL INFORMATION:

APPLICANT: Mark D. Cochran

TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,459

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Beq, John P.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 4177 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 115..1860  
NAME/KEY: CDS  
LOCATION: 2095..3756  
US-08-477-459-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75  
DB 2064 TCGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123  
QY 76 AGCACCCTATGATCTGATCTATCCGGGTGGCTGGCACTGAGTTGCACTGTCCGGCAAA 135  
DB 2124 AGCACCCTATGATCTGATCTATCCGGGTGGCTGGCACTGAGTTGCACTGTCCGGCAAA 2183  
QY 136 CTCATTTGATGGCAGGCTCTTTCAGCTGCGAGAAATTTGTGTTACAGAGAACAAAGCCGT 195  
DB 2184 CTCATTTGATGGCAGGCTCTTTCAGCTGCGAGAAATTTGTGTTACAGAGAACAAAGCAGT 2243  
QY 196 CAACATTAACCTCACTCCAGACAGGATCAATCATAGTTAGCTCCTCCGAATCTGCC 255  
DB 2244 CAACATTAACCTCACTCCAGACAGGATCAATCATAGTTAGCTCCTCCGAATCTGCC 2303  
QY 2244 CAACATTAACCTCACTCCAGACAGGATCAATCATAGTTAGCTCCTCCGAATCTGCC 2303  
DB 2244 CAACATTAACCTCACTCCAGACAGGATCAATCATAGTTAGCTCCTCCGAATCTGCC 2303  
QY 256 CAAGATTAAGAGAGCATGTGCGAAAGCCCTTGGATGATCAATCAAGACAGATTTGACAC 315  
DB 2304 AAAGATTAAGAGAGCATGTGCGAAAGCCCTTGGATGATCAATCAAGACAGATTTGACAC 2363  
QY 316 TTGCTGACCCCTTGGTGTGATCTTATCCGTAGAAATCAAGAGTCTGTGATCATCTGG 375  
DB 2364 TTGCTGACCCCTTGGTGTGATCTTATCCGTAGAAATCAAGAGTCTGTGATCATCTGG 2423  
QY 376 AGGGGGGAGACAGGGGCGCTTATAGCGCATTAATGGCGGTGGCTTGGGGGTGC 435  
DB 2424 AGGGGGGAGACAGGGGCGCTTATAGCGCATTAATGGCGGTGGCTTGGGGGTGC 2483  
QY 436 AACTGCCGCAAAATTAACAGCGGCGCAGCTGATATCAAGCCAAACAAATCTGCAAA 495  
DB 2484 AACTGCCGCAAAATTAACAGCGGCGCAGCTGATATCAAGCCAAACAAATCTGCAAA 2543  
QY 496 CATCTCCGACTTAAGAGAGCATTTGCCGCAACCAATGAGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAGAGAGCATTTGCCGCAACCAATGAGCTGTGATGAGTCACTGA 2603  
QY 556 CGGATTAATGCAACTAGCAGTGGCAATTTGGGAAGATGCGACGTTTGTATACCAATT 615  
DB 2604 CGGATTAATGCAACTAGCAGTGGCAATTTGGGAAGATGCGACGTTTGTATACCAATT 2663  
QY 616 TAATTAACAGCTCAGAAATTTAGCTGATCAATTAATTTGACAGCAAGTTGTGTAGAGCT 675  
DB 2664 TAATTAACAGCTCAGAAATTTAGCTGATCAATTAATTTGACAGCAAGTTGTGTAGAGCT 2723  
QY 676 CAACCTGTACTAACCGAATTTGACTACAGTATTCGAGCAACCAATCACTTCACTGCTTT 735  
DB 2724 CAACCTGTACTAACCGAATTTGACTACAGTATTCGAGCAACCAATCACTTCACTGCTTT 2783  
QY 736 AAACAAGCTGACTTAATCAAGCACTTTAACAATCTAGCTGTGGGAATTAATGATTAATAT 795  
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QY 796 GACTTAAGTTAGGTGAGGAAACAATCAATCACTCACTGATTAATGAGGCTTAATCAC 855  
DB 2844 GACTTAAGTTAGGTGAGGAAACAATCAATCACTCACTGATTAATGAGGCTTAATCAC 2903  
QY 856 CGGTAAACCTTAATCTATACGACTCAGAGACTCAACTCTTGGGTATACAGGTAACTCTAAC 915

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Db      2964 TTGAGTGGGGAACCTTAATATATGCGGCAACCTACTGGAAACCTTATCCGTAGAC 3023
Qy      976  AACGAGGGAATTTGCTCGGCACTTGTCCTCAAAAGTGGAACAGAGTGGTTCGTGAT 1035
Db      3024 AACGAGGGAATTTGCTCGGCACTTGTCCTCAAAAGTGGAACAGAGTGGTTCGTGAT 3083
Qy      1036 AGAAGAACTTGACACTCTCATCTGTATAGAACTGACTTATGATTATTTGTAACAGAT 1095
Db      3084 AGAAGAACTTGACACTCTCATCTGTATAGAACTGACTTATGATTATTTGTAACAGAT 3143
Qy      1096 AGTAACTTCCCTATGTCCTGCTGATTTATCTGCTGAGCGGCAATAGTGGGCTG 1155
Db      3144 AGTAACTTCCCTATGTCCTGCTGATTTATCTGCTGAGCGGCAATAGTGGGCTG 3203
Qy      1156 TATGTACTCAAAAGACCGAAGCGCACTTACTACACATACATGACTATCAAGGTTCACT 1215
Db      3204 TATGTACTCAAAAGACCGAAGCGCACTTACTACACATACATGACTATCAAGGTTCACT 3263
Qy      1216 CATGCCAACTGCAAGATGACAAATGATGATGATGATGATGATGATGATGATGATGAT 1275
Db      3264 CATGCCAACTGCAAGATGACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 3323
Qy      1276 AAATCTATGAGAGAACCGGTCTCTATATGATATGATATGATATGATATGATATGATATGAT 1335
Db      3324 AAATCTATGAGAGAACCGGTCTCTATATGATATGATATGATATGATATGATATGATATGAT 3383
Qy      1336 CGGATTAACCTTAAAGGCTCAGTGGGGAATTTGATGATGATGATGATGATGATGATGATGAT 1395
Db      3384 CGGATTAACCTTAAAGGCTCAGTGGGGAATTTGATGATGATGATGATGATGATGATGATGAT 3443
Qy      1396 ACAAGATTTCTCAAGTATATATACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db      3444 ACAAGATTTCTCAAGTATATATACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 3503
Qy      1456 CAACAACTCCGATCGATATGCTTGAATATGATGATGATGATGATGATGATGATGATGAT 1515
Db      3504 CAACAACTCCGATCGATATGCTTGAATATGATGATGATGATGATGATGATGATGATGAT 3563
Qy      1516 AGTCAATGTCAAAGCTAGACATCGCTCTCATTAACCTATATCGTTGATGATGATGAT 1575
Db      3564 AGTCAATGTCAAAGCTAGACATCGCTCTCATTAACCTATATCGTTGATGATGATGAT 3623
Qy      1576 ATCTCTGTTTTGGTATTAAGCTGATCTAGATGCTACATGCTAATGTAACAAGCAAA 1635
Db      3624 ATCTCTGTTTTGGTATTAAGCTGATCTAGATGCTACATGCTAATGTAACAAGCAAA 3683
Qy      1636 GGGGCAACAAAAAAGCTTATATGCTTGGGAATATATCTGATGATGATGATGATGATGATGAT 1695
Db      3684 GGGGCAACAAAAAAGCTTATATGCTTGGGAATATATCTGATGATGATGATGATGATGATGAT 3743
Qy      1696 TACAAAAATGGAACAGATGAGGAAGGTTCCCTAATGTAATTTGTTGGAAG 1755
Db      3744 TACAAAAATGGAACAGATGAGGAAGGTTCCCTAATGTAATTTGTTGGAAG 3803
Qy      1756 TTCTGTAGTCTGTCAGTTCAAGAGTTAAGAAAAA 1792
Db      3804 TTCTGTAGTCTGTCAGTTCAAGAGTTAAGAAAAA 3840

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RESULT 5
US-08-479-869-12
: Sequence 12, Application US/08479869
: Patent No. 6123949
: GENERAL INFORMATION:
: APPLICANT: Cochran Ph.D, Mark D
: TITLE OF INVENTION: Recombinant Fowlpox Virus S-PPV-043 and
: TITLE OF INVENTION: Uses thereof
: NUMBER OF SEQUENCES: 20

```

```

CORRESPONDENCE ADDRESS:
: ADDRESS: John P. White
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/479,869
: FILING DATE:
:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/024,156
: FILING DATE: 26-FEB-1993
:
: ATTORNEY/AGENT INFORMATION:
: NAME: White Esq, John P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
:
: TELETYPE: 422523
:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4177 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 115..1860
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 2095..3756
:
: US-08-479-869-12
:
: Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
: Best Local Similarity 98.8%; Pred. No. 0;
: Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY	436	AACTGCGCGCAAAATTAACAGCGCGCGAGCTTGATTAACAGCGCAAAACAAAATGCTGCCAA	495
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QY	486	CATCTCGCACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGTGCATGAGGTCACTGA	555
Db	2544	CATCTCGCACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGTGCATGAGGTCACTGA	2603
QY	556	CGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCGTTGTATATGACCAATT	615
Db	2604	CGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCGTTGTATATGACCAATT	2663
QY	616	TAATTAACAGCTGACGAATTAGATCTGCATTCAAAATTGCACAGCAAGTTGGTGTAGACT	675
Db	2664	TAATTAACAGCTGACGAATTAGATCTGCATTCAAAATTGCACAGCAAGTTGGTGTAGACT	2722
QY	676	CAACCTGTACTTAACCGAATTGACTACTAGTATTCGGACCAACAAATCACTTCACTGCTT	735
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Db	2784	AAACAGCTGACTATTTCAGGCACTTTACATCTAGCTGTGGAAAATATGATTACTTATT	2843
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Db	2844	GACTTAAGTTAGGTGTAGGGAAACAATCACTCAGCTCATTTAATCGTAGCGCTTAATCAAC	2903
QY	856	CGGTAAACCTATTCTTATACGACTCAGACACTCACTCTTGGGTATACAGGTAACTTACC	915
Db	2904	CGGTAAACCTATTCTTATACGACTCAGACACTCACTCTTGGGTATACAGGTAACTTACC	2963
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Db	3024	AAACGAGGGATTTGCTCGCGCACTTGTCCCAAAAGTGTGACACAGTTCGTTCTGTAT	3083
QY	1036	AGAAACCTTGAACCTCACTGATGTATAGAAACCTAGTTATATTTGTAACAAGAT	1095
Db	3084	AGAAACCTTGAACCTCACTGATGTATAGAAACCTAGTTATATTTGTAACAAGAT	3143
QY	1096	AGTAAAGTTCCCTATGTCCCTCGTATATTATTCCTTGAACGGCAATACGTGGGCTGT	1155
Db	3144	AGTAAAGTTCCCTATGTCCCTCGTATATTATTCCTTGAACGGCAATACGTGGGCTGT	3203
QY	1156	TATGTACTCAAAAGACCGAAGGGGCACTTAACACATACATGACTATCAAAAGTTCACT	1215
Db	3204	TATGTACTCAAAAGACCGAAGGGGCACTTAACACATACATGACTATCAAAAGTTCACT	3263
QY	1216	CATGCGCAACCTGCAAGATGACAAACATGTAGATGTGAAACCCCGGGGATCATATGCGA	1275
Db	3264	CATGCGCAACCTGCAAGATGACAAACATGTAGATGTGAAACCCCGGGGATCATATGCGA	3323
QY	1276	AAACTATGAGAAAGCCGTGTCTCTATATGATTAACAATCATGCAATGTTTTATCCTTAGG	1335
Db	3324	AAACTATGAGAAAGCCGTGTCTCTATATGATTAACAATCATGCAATGTTTTATCCTTAGG	3383
QY	1336	CGGATTAACCTTTAAGGCTCAGTGGGGAATTGCATTAACCTTATCAGAAATATTTCAAT	1395
Db	3384	CGGATTAACCTTTAAGGCTCAGTGGGGAATTGCATTAACCTTATCAGAAATATTTCAAT	3443
QY	1396	ACAAGATTCTCAAGTAATTAATTAACAAGGAATCTTGATATCTCAATGAGCTTGGGAATGT	1455
Db	3444	ACAAGATTCTCAAGTAATTAATTAACAAGGAATCTTGATATCTCAATGAGCTTGGGAATGT	3503
QY	1456	CAACAACCTGCATCAGATAATGCTTTGTAATTAAGTTAAGAAAGCAACAAAACTTGACAA	1515
Db	3504	CAACAACCTGCATCAGATAATGCTTTGTAATTAAGTTAAGAAAGCAACAAAACTTGACAA	3563

QY	1516	AGTCAATGTCAAACCTGACTAGACACATCTGCTCTCATTAACCTATTCGTTTGGACATCAT	15175
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QY	1636	GGCGCAACAAACAAACCTTATATTAGCTTTGGAAATATATCTTAGATCATGATGAGGCCAC	16959
DB	3684	GGCGCAACAAACAAACCTTATATTAGCTTTGGAAATATATCTTAGATCATGATGAGGCCAC	37434
QY	1696	TACAAAATATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATGTATTTGTGTGAAG	17555
DB	3744	TACAAAATATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATGTATTTGTGTGAAG	38033
QY	1756	TTCTGTATGTCGTCTGACGTTCCGAGATTAAGTAAGAAACAA 1792	
DB	3804	TTCTGTATGTCGTCTGACGTTCCGAGATTAAGTAAGAAACAA 3840	
RESULT 6			
US-08-486-414-12			
; Sequence 12, Application US/08486414B			
; Patent No. 6136318			
; GENERAL INFORMATION:			
; APPLICANT: Cochran, Mark D.			
; APPLICANT: Junker, David E.			
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF			
; FILE REFERENCE: 42771D			
; CURRENT APPLICATION NUMBER: US/08/486,414B			
; CURRENT FILING DATE: 1995-06-07			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 12			
; LENGTH: 4177			
; TYPE: DNA			
; ORGANISM: Fowlpox virus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (115)..(1857)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (2095)..(3753)			
US-08-486-414-12			
Query Match			
Best Local Similarity 51.9%; Score 1741.8; DB 3; Length 4177;			
Matches 1755; Conservative % 0; Mismatches 22; Indels 0; Gaps 0;			
QY	16	TGATATCCCGGTGGCGCCCTCCAGGTCCAAAGATGGGCTCCAGACCTTCTACCAAGAACCC	75
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QY	76	AGCACTATGATGTGTAAGTATCCGGGTTGCGCTGGACCTGAGTGGCATCTGTCCGCAAA	135
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QY	136	CTCCATTTGATGGCAGGCGCTCTTGCAGCTGCAAGAAATTTGGTTACAGAGACAAAGCCGT	195
DB	2184	CTCCATTTGATGGCAGGCGCTCTTGCAGCTGCAAGAAATTTGGTTACAGAGACAAAGCAGT	22433
QY	196	CAACATATTAACCTCATATCCACAGACAGATCAATATGTTAAGTCTCTCCGAAATCTGCC	255
DB	2244	CAACATATTAACCTCATATCCACAGACAGATCAATATGTTAAGTCTCTCCGAAATCTGCC	23033
QY	256	CAAGAAATTAAGGAGCATGTGCGAAAGGCCCTTGGATGCAATACAAACAGACATTGACAC	315
DB	2304	CAAGAAATTAAGGAGCATGTGCGAAAGGCCCTTGGATGCAATACAAACAGACATTGACAC	23633
QY	316	TTTGTCTACCCCTTGTGTGATCTATTCGTAAGATACAAAGATCTGTGACTACATCTGG	375
DB	2364	TTTGTCTACCCCTTGTGTGATCTATTCGTAAGATACAAAGATCTGTGACTACATCTGG	24233

QY 376 AGGGGGGAGACAGGGGGCCCTTATAGCGCCATTATGGCGGTGTGCTTTGGGGTTC 435  
DB 2424 AGGGGGGAGACAGGGGGCCCTTATAGGGCCATTATGGCGGTGTGCTTTGGGGTTC 2483  
QY 436 AACTGCGCACAAATTAACAGCGCGCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA 495  
DB 2484 AACTGCGCACAAATTAACAGCGCGCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA 2543  
QY 496 CATCTCCGACTTAAAGAGACATTTCCGCAACCAATGAGCTGTGATGAGTCACTGA 555  
DB 2544 CATCTCCGACTTAAAGAGACATTTCCGCAACCAATGAGCTGTGATGAGTCACTGA 2603  
QY 556 CGGATTAACGCAATGAGAGTGGAGTGGGAAGTGCAGAGTTTGTAAATGACCAAT 615  
DB 2604 CGGATTAACGCAATGAGAGTGGAGTGGGAAGTGCAGAGTTTGTAAATGACCAAT 2663  
QY 616 TAATTAACAGCTCAGGAATTAAGCTGCATCAAAATTTGCACAGCAAGTTGTGTAGACT 675  
DB 2664 TAATTAACAGCTCAGGAATTAAGCTGCATCAAAATTTGCACAGCAAGTTGTGTAGACT 2723  
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QY 796 GACTAAGTATGATGAGGAACAATCAACAGCTCATTAATCGGTAGCGGCTTAATCAG 855  
DB 2844 GACTAAGTATGATGAGGAACAATCAACAGCTCATTAATCGGTAGCGGCTTAATCAG 2903  
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DB 3144 AGTAACGTTCCCTATGTCCTCGATTAATTTCCGCTTGAAGCGGCATTAAGCGGCTG 3203  
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DB 3264 CATGCGCAACTGCAAGATGACAACTGTATGTGTAACCCCGGGTATCATATGCCA 3323  
QY 1276 AAATCTATGAGAGCGCGTGTCTCTAATAGATTAACAAATCAAGCAATGTTTATCCTTAGG 1335  
DB 3324 AAATCTATGAGAGCGCGTGTCTCTAATAGATTAACAAATCAAGCAATGTTTATCCTTAGG 3383  
QY 1336 CGGGATACTTTAAGGCTCAGTGGGGAATTCGATTAATCTTATCAGAGAAATATCTCAT 1395  
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QY 1396 ACAAGATTTCTCAAGATTAATTAACAGGCAATTTGATATCTCACTGAGCTTGGGAATGT 1455  
DB 3444 ACAAGATTTCTCAAGATTAATTAACAGGCAATTTGATATCTCACTGAGCTTGGGAATGT 3503

QY 1456 CAACAATCGATCAGTATGCTTTGAATTAAGTAAAGCAACAGAAACTAGACAA 1515  
DB 3504 CAACAATCGATCAGTATGCTTTGAATTAAGTAAAGCAACAGAAACTAGACAA 3563  
QY 1516 AGTCAATGTCAAACTGACATGACATGCTCTCATTAATCTATGCTTTGACTATCAT 1575  
DB 3564 AGTCAATGTCAAACTGACATGACATGCTCTCATTAATCTATGCTTTGACTATCAT 3623  
QY 1576 ATCTCTGTTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635  
DB 3624 ATCTCTGTTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3683  
QY 1636 GGGCCAAACAAAACCTTATTAATGCTTGGGAATTAATTAATTAATTAATTAAT 1695  
DB 3684 GGGCCAAACAAAACCTTATTAATGCTTGGGAATTAATTAATTAATTAATTAATTAAT 3743  
QY 1696 TACAAAATGTGAACACAGATGAGAAACGAAGTTTCCCTAATATGATTAATTTGTGAAAG 1755  
DB 3744 TACAAAATGTGAACACAGATGAGAAACGAAGTTTCCCTAATATGATTAATTTGTGAAAG 3803  
QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792  
DB 3804 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 3840

RESULT 7  
PCT-US94-01826A-12  
; Sequence 12, Application PC/TUS9401826A  
; GENERAL INFORMATION:  
; APPLICANT: Syntro Corporation, et al.  
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01826A  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Beq, John P.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 115..1860  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2095..3756  
; PCT-US94-01826A-12  
Query Match 51.9%; Score 1741.8; DB 6; Length 4177;  
Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Db 2064 TCGATCCGGTGGCCCTTCAAGTGCAGATGCGCTCCAGACCTTCTACCAAGAACCC 2123
QY 76 AGCACTTATATGCTGATATCCGGGTGGCGTGGCATCTGAGTTGCAATCTGTCCGGCAA 135
Db 2124 AGCACTTATATGCTGATATCCGGGTGGCGTGGCATCTGAGTTGCAATCTGTCCGGCAA 2183
QY 136 CTCATTGATGAGGAGGCTCTTGAGCTGAGAAATTTGGTTACAGAGACAAAGCCGT 195
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QY 196 CAACATATACACTTATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC 255
Db 2244 CAACATATACACTTATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC 2303
QY 256 CAAGATPAGAGAGGATGTGCGAAAGCCCTTGGATGCATPACACAGACATTGACAC 315
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QY 316 TTGCTCAACCCCTTGGTGACTCATCCGTAGGATACAGAGTCTGATCATCATCTGG 375
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QY 436 AACTGCCGACAAATACAGCGGCGCGACTGTGATACAGCCAAACAAATGCTGCCAA 495
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QY 1036 AGAAGAACTTGACACTTCTATCTGTATAGAAAGTGAAGTCTTATATTTATGTAACAAGAT 1095
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QY 1396 ACAAGATTTCAAGTATTAATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db 3444 ACAAGATTTCAAGTATTAATTAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 3503
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Db 3804 TTCTGTAGTCTGTCACTGAGAGTTAAGAAAAA 3840
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RESULT 8
PCT-US94-02252A-12
; Sequence 12, Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
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ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 115..1860
NAME/KEY: CDS
LOCATION: 2095..3756
PCT-US94-02252A-12

Query Match      51.9%; Score 1741.8; DB 6; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGGCTCCAGACCTTTACCAAGAACCC 75
Db 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGGCTCCAGACCTTTACCAAGAACCC 2123
QY 76 AGCACTATGATGCTGATCTATCCGGGTGCGCTGGCACTGATTCATCTGTCGGGCAAA 135
Db 2124 AGCACTATGATGCTGATCTATCCGGGTGCGCTGGCACTGATTCATCTGTCGGGCAAA 2183
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QY 976 AACCAAGGGATTTGCTCGGCACTTTGTCCAAAGTGTGACACAGGTGCGTCTGTGAT 1035
Db 3024 AACCAAGGGATTTGCTCGGCACTTTGTCCAAAGTGTGACACAGGTGCGTCTGTGAT 3083
QY 1036 AGAAGAACTTGACACCTCATCTGTATATGAAACCTGACTTAGATTATATTTGACAAAGAT 1095
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QY 1096 AGTAACGTTCCCTATATGTCCTCGTATTTATTCCTGCTTGAAGCGGCAATAGTCGGCCTG 1155
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QY 1156 TATGTACTCAAAAGACCGAAGCGCACTTATACACCATATGACTATCAAAAGTTCACT 1215
Db 3204 TATGTACTCAAAAGACCGAAGCGCACTTATACACCATATATGACTATCAAAAGGCTCAGT 3263
QY 1216 CATGGCCAACTGCAAGATGACAAACATGTATGTATTAACCCCGGGTATCATATGCA 1275
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Db 3744 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTAATATGTAATTTGTGAAG 3803
QY 1756 TTTCTGTATGCTGTCAAGTTCAAGAGATTAAGAAAAA 1792
Db 3804 TTTCTGTATGCTGTCAAGTTCTGAGAGTTTAAGAAAAA 3840
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RESULT 9
US-09-881-457A-1
; Sequence 1, Application US/09881457A
; Patent No. 6913751
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. 6913751el Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1OKOK
; CURRENT APPLICATION NUMBER: US/09/881,457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
US-09-881-457A-1

Query Match      50.7%; Score 1701.6; DB 3; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

QY      16 TGGATCCGCGTGGCGCCCTTCAGAGTGCAAGATGGGCTCCAGACCTTCTACCAAGAAACC 75
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QY      136 CTCATTGATGGGCGGCGCTCTTGAGCTGAGAAATGTGGTTACAGGAGCAAAAGCGT 195
DB      1319 CTCATTGATGGGCGGCGCTCTTGAGCTGAGAAATGTGGTTACAGGAGCAAAAGCGT 1377
QY      196 CAACATATAGACCTCATCTCCAGACAGATCAATCATATGTTAAGCTCTCCCGAATCTGCC 255
DB      1378 CAACATATAGACCTCATCTCCAGACAGG-TCAATCATATTTAAGCTCTCCCGAATCTGCC 1435
QY      256 CAAGGATAGAGGAGCATGTGGGAAAGCCCTTGGATGCATACAAAGACATTGACCAAC 315
DB      1436 AAAGGATAGAGGAGCATGTGGGAAAGCCCTTGGATGCATACAAAGACATTGACCAAC 1495
QY      316 TTGGCTACACCCCTTGGTGACTCTATCCGTAGGATCAAGAGCTGTGACTATCATCTGG 375
DB      1496 TTGGCTACACCCCTTGGTGACTCTATCCGTAGGATCAAGAGCTGTGACTATCATCTGG 1555
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DB      1676 CATCTCCGACTTAAAGAGGCAATTCGCGCAACCAATGAGCTGTGCATGAGTCACTGA 1735
QY      556 CGGATTAATGCAATTAAGAGTGGGAGATGCGAAGATGCAAGTGTGTATGACCAATT 615
DB      1736 CGGATTAATGCAATTAAGAGTGGGAGATGCGAAGATGCAAGTGTGTATGACCAATT 1795
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QY      1216 CATGCGCAACTGCAAGATGACCAATGATGATGTTAAACCCCGGGGTATCATATGCA 1275
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QY      1336 CGGGATTAATTTAAGGTCAGTGGGAAATTCATGTAATCTTAACAGAAATATCTCAAT 1395
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QY      1396 ACAAGATTTCAAGTAAATTAATTAACAGGCAATCTTGAATCTCAACTGAGCTTGGGAATGT 1455
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QY      1456 CAACAACTGATCAGTAATGCTTTGAATTAATGAGAAAGCAACAGAAACTTAGACAA 1515
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Db 2636 CAACACCTCGATCGATGATGCTTGAATTAAGTTAGAGAAAGCAACAGAAAACTTAGCAA 2695  
Qy 1516 AGTCAATGTCAAACTGATGACATCGCTCTCATTAACCTATATCGTTTGACATCAT 1515  
Db 2696 AGTCAATGTCAAACTGATGACATCGCTCTCATTAACCTATATCGTTTGACATCAT 2755  
Qy 1576 ATCTCTGTTTTGGTACTACTAGCTGATTTCTAGCATGCTACTAATGTACAAGCAAAA 1635  
Db 2756 ATCTCTGTTTTGGTACTACTAGCTGATTTCTAGCATGCTACTAATGTACAAGCAAAA 2815  
Qy 1636 GGGCGCAACAAAACTTATTTATGCTTGGGAATPATCTTAATCATGATGAGAGCCAC 1695  
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Qy 1696 TACAAAATGTGACACAGATGAGAAAGGATTTCCCTAATAGTATTTGTGGAAG 1755  
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Qy 1756 TTCTGTAGTCTGTCACTTCAAGAGTTAAAGAAAAA 1792  
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RESULT 10  
US-08-663-566A-12  
Sequence 12, Application US/08663566A  
Patent No. 5853733

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D

APPLICANT: Macdonald, Richard D

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

TITLE OF INVENTION: and Uses Thereof

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/663,566A

FILING DATE: June 13, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

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TELEFAX: (212) 391-0526

TELEX: 422523

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1662 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1662

US-08-663-566A-12

Query March 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;

Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 47 ATGGGCTCCAGACCTTCTACCAAGACCAGACCTATGATGCTGACTATCCGGGTGCG 106  
Db 1 ATGGGCTCCAGACCTTCTACCAAGACCAGACCTATGATGCTGACTATCCGGGTGCG 60  
Qy 107 CTGGACCTGAGTTGCACTCTGTCGGGCAAACTCCATTGATGGCAGGCGCTTGGCACTGCA 166  
Db 61 CTGGACTGAGTTGCACTCTGTCGGGCAAACTCCATTGATGGCAGGCGCTTGGCACTGCA 120  
Qy 167 GGAATGGGTGTTACAGAGACCAAGCCGTCAACATATACCTCATCCAGACAGATCA 226  
Db 121 GGAATGGGTGTTACAGAGACCAAGCCGTCAACATATACCTCATCCAGACAGATCA 180  
Qy 227 ATCATAGTTAAGCTCTCCGGAATCTGCCAAGATGAGAGGAGATGTCGAAAGCCGCC 286  
Db 181 ATCATAGTTAAGCTCTCCGGAATCTGCCAAGATGAGAGGAGATGTCGAAAGCCGCC 240  
Qy 287 TTGGATGATTCACACAGACATTGACCACTTGTCTACCCCTTGGTGACTCTATCCGT 346  
Db 241 TTGGATGATTCACACAGACATTGACCACTTGTCTACCCCTTGGTGACTCTATCCGT 300  
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Db 301 AGGATACAGAGCTGTGACCTACATCTGAGGGGGGAGACAGGGGGCGCTTATAGGGGCC 360  
Qy 407 ATTATTTGGCGGTGTGGCTCTTGGGGTTGCAACTCCCGACAAATATACAGCGCGCAGCT 466  
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Qy 467 CTGATACAGGCAAAATATGCTGCAACATCTCTCGACTTAAAGAGAGATTTGCCCA 526  
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Qy 527 ACCAATGAGGCTGTGACATGAGTCACTGACGATTAATCGCAACTAGAGATGGCGTTGG 586  
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Qy 767 CTAGCTGGTGAATATGATGATTACTTAATGACTAAGTTAGGTAGGGAACAATCAATC 826  
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Qy 827 AGCTCATTAATCGGTAGCGGCTTATACACCGGTAACTTATAGACTCAAGACT 886  
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Qy 887 CAATCTTTGGGTATACAGTATCTTACCTTCACTGAGTGGGAACTTAATATCGGTGCC 946  
Db 841 CAATCTTTGGGTATACAGTATCTTACCTTCACTGAGTGGGAACTTAATATCGGTGCC 900  
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Qy 1067 ACTGACTTAATTTATTTGATGACAAATATGATTAAGTTCCCTTATGTCCTCGGTATTTAT 1126  
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QY 1127 TCCTGCTTGAAGCGGCAATACGTGCGGCTGTATGTACTCAAGACGGAAGCGGCACTTACT 1186
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QY 1187 ACACCATACATGATATCAAAAGGTTCACTCATCGCCCACTGCAAGATGACAACTGTGGA 1246
DB 1141 ACACCATATATGACTATCAAAAGGCTCAGTCAATCGCTCAAGATGACAACTGTGGA 1200
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DB 1201 TGATTAACCCCGGGGATCATATCGCAAAACTATGAGAGAGCGGTCTCTAATAGAT 1260
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DB 1261 AAACCAATCATGCAATGTTTTATCCTTAGCGGGGATTAACCTTAGGCTCAGTGGGAAATTC 1320
QY 1367 GATGTAACTTATCAAGAAATATCTCAATACAAATTTCTCAAGTAAATATACAGGCAT 1426
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QY 1427 CTGATATCTCAACTGAGCTGGGAATGTCAACAACCTGATCAGTAAATGCTTGAATAG 1486
DB 1381 CTGATATCTCAACTGAGCTGGGAATGTCAACAACCTGATCAGTAAATGCTTGAATAG 1440
QY 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACATCTGCT 1546
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DB 1501 CTCAATTAACCTATATCGTTTGAATCAATATCTCTGTTTTTGGTAAATCTTAACTGAT 1560
QY 1607 CTAGCATGCTACCTAATGTAACAGCAAAAGCGCAACAAAACCTTATTATGCTTGGG 1666
DB 1561 CTAGCATGCTACCTAATGTAACAGCAAAAGCGCAACAAAACCTTATTATGCTTGGG 1620
QY 1667 AATAATCTCTAGATCAGATGAGAGCCATCAAAAATGTGA 1708
DB 1621 AATAATCTCTAGATCAGATGAGAGCCATCAAAAATGTGA 1662

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RESULT 11
US-08-023-610-12
; Sequence 12, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; APPLICANT: Macdonald Ph.D., Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSES: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
;

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; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
;
US-08-023-610-12

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Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTCG 106
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTCG 60
QY 107 CTGGCACTGAGTGCATCTGTCCGGCAACTCCATTGATGAGCGGCTTTGACAGCTGA 166
DB 61 CTGGTACTGAGTGCATCTGTCCGGCAACTCCATTGATGAGCGGCTTTGACAGCTGA 120
QY 167 GGAATGTGTTACAGAGACAAAGCCGTCACATATACACTATCCAGACAGATCA 226
DB 121 GGAATGTGTTACAGAGACAAAGCGTCAACTATACCTCATCCAGACAGATCA 180
QY 227 ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGATTAAGGAGCATGTGGAAGCCCC 286
DB 181 ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGATTAAGGAGCATGTGGAAGCCCC 240
QY 287 TTGGATGCAATACACAGAGATTGACCACTTGTCTACCCCCCTTGTGATCTATCCGT 346
DB 241 TTGGATGCAATACACAGAGATTGACCACTTGTCTACCCCCCTTGTGATCTATCCGT 300
QY 347 AGGATCAAGAGTCTGTGACTATCATCTGAGGGGGAGACAGGGGGCCTTATAGGGCC 406
DB 301 AGGATCAAGAGTCTGTGACTATCATCTGAGGGGGAGACAGGGGGCCTTATAGGGCC 360
QY 407 ATTATGGCGGTGTGGCTCTTGGGGTTGCACTGCGGCAAAATTAACGCGCGCAGCT 466
DB 361 ATTATGGCGGTGTGGCTCTTGGGGTTGCACTGCGGCAAAATTAACGCGCGCAGCT 420
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DB 421 CTGATACAGCCCAAAATGCTGCCCAATCTCTCCGACTTAAAGAGACATTGCCGA 480
QY 527 ACCAATGAGCTGATGATGAGTCACTGACGATTAACGCACTAGACAGTGGAGTTGGG 586
DB 481 ACCAATGAGCTGATGATGAGTCACTGACGATTAACGCACTAGACAGTGGAGTTGGG 540
QY 587 AAGATGAGCAGTTTGTAAATGAACAATTTAATAAACAAGCTCAGGAATTAGACTGATC 646
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QY 707 TTGGAGCAACAATCACTTCACTGCTTTAAACAAGTGACTATTAGGACCTTTACAAT 766
DB 661 TTGGAGCAACAATCACTTCACTGCTTTAAACAAGTGACTATTAGGACCTTTACAAT 720
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DB 721 CTAGCTGTGGAATATGATTAATTAATGATTAAGTATGATGAGGAAATCAATCACTC 780
QY 827 AGCTCATTAATCGGTAGCGGCTTAATCAACGGTAACCTATTATTATACACTACAGACT 886

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Db 781 AGCTCATTAATCGGTAGCGGCTTAATACCGGTAACTTATTTACTACACTCACAGACT 840  
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Db 841 CAACCTTGGGTATACAGGTAACTTACTTCACTGCGGAACTTAATATATATGGTGCC 900  
Qy 947 ACTTACTTGGAAACCTTATCCGTAAAGCAACAGGGGATTTGCTCGGCACTTGTCCTCA 1006  
Db 901 ACTTACTTGGAAACCTTATCCGTAAAGCAACAGGGGATTTGCTCGGCACTTGTCCTCA 960  
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Qy 1067 ACTGACTTGAATTTATTTATTTGACAAAGATTAAGTTCCTTATGTCCTGCTGATTTAT 1126  
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Db 1081 TCCTGCTTGAAGCGGCAATACGTCGGCTGTATGTATCAAAAGACCGAAGCGCACTTACT 1140  
Qy 1187 AACACATACAGACATATACAAAGTTCAGTCACTGCGCACTGCAAGATGACAAACATGTA 1246  
Db 1141 AACACATATATGACTATACAAAGTTCAGTCACTGCGCACTGCAAGATGACAAACATGTA 1200  
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Db 1201 TGTGTAAACCCCGGGATGATATATCGAAACATATGAGAAAGCGGTCTCTCTATATAGAT 1260  
Qy 1307 AAACATATACGAAATGTTTATCTTTAGCGGGATTAACCTTAAAGCTCAGTGGGAAATTC 1366  
Db 1261 AAACATATACGAAATGTTTATCTTTAGCGGGATTAACCTTAAAGCTCAGTGGGAAATTC 1320  
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Db 1381 CTGATATCTCAAGCTGAGCTTGGGAATGTCAAACATCGATCAGTATGCTTGAATAG 1440  
Qy 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACATCTGCT 1546  
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Qy 1607 CTACATGCTTACCTTAATGTAAGAAAGCGCAAAACCTTATTAAGCTTGGG 1666  
Db 1561 CTACATGCTTACCTTAATGTAAGAAAGCGCAAAACCTTATTAAGCTTGGG 1620  
Qy 1667 AATATATCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1708  
Db 1621 AATATATCTTATGATCAGATGAGAGCCACTACAAAAATGTGA 1662

RESULT 12  
US-08-288-065A-12  
Sequence 12, Application US/08288065A  
Patent No. 5961982

GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Macdonald, Richard D  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,065A  
FILING DATE: Aug-09-94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1662 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1662  
US-08-288-065A-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;

Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 47 ATGGGCTTCAGACCTTCTTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGCG 106  
Db 1 ATGGGCTTCAGACCTTCTTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTGCG 60  
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Qy 1607 CTAGCATGTACTAATGTATCAACAAAGGCGCAACAAAACCTTATTAATGCTTGGG 1666  
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Qy 1667 AATTAATCTTGAATGATGAGAGCACTTAACAAAATGTA 1708

Db 1621 AATTAATCTTGAATGATGAGAGCACTTAACAAAATGTA 1662  
RESULT 13  
US-08-362-240A-12  
Sequence 12: Application US/08362240A  
Patent No. 5965138  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Junker, David  
APPLICANT: Wild, Martha A  
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,240A  
FILING DATE: Dec-22-94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0400  
TELEFAX: (212)391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1662 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1662  
US-08-362-240A-12  
Query Match 48.6%; Score 1631.6; DB 2; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTCCG 106  
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTCCG 60  
Qy 107 CTGGCACTGAGTGTGATCTGTCCGGGCAAACTCCATTTGATGAGGAGCCCTTTGACGCTGA 166  
Db 61 CTGGTACTGAGTGTGATCTGTCCGGGCAAACTCCATTTGATGAGGAGCCCTTTGACGCTGA 120  
Qy 167 GGAATTGTGTTACAGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCA 226  
Db 121 GGAATTGTGTTACAGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCA 180  
Qy 227 ATCATAGTTAAGCTCTCCGGAATCTGCCCCAAGATTAAGGAGCATGTGGAAGCCCC 286  
Db 181 ATCATAGTTAAGCTCTCCGGAATCTGCCCCAAGATTAAGGAGCATGTGGAAGCCCC 240  
Qy 287 TTGGATGCAATACAACAGAGATTTGACCACTTTGTCTACCCCCCTTGTGATCTATTCGT 346  
Db 241 TTGGATGCAATACAACAGAGATTTGACCACTTTGTCTACCCCCCTTGTGATCTATTCGT 300

QY 347 AGATACAAAGTCTGTGCTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCC 406  
DB 301 AGGATACAAAGTCTGTGCTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCC 360  
QY 407 ATTATTTGGGGGCTCTTGGGGGTTGCACTGCGGCAATAATACAGCGGCGGCACT 466  
DB 361 ATTATTTGGGGGCTCTTGGGGGTTGCACTGCGGCAATAATACAGCGGCGGCACT 420  
QY 467 CTGATACAAAGCAAAATGCTCCCAACATCTCCGACTTAAAGAGAGCATTCGCCA 526  
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QY 527 ACCAATGAGGCTGTGCTAGAGGTCACTGAGGATTTACGCACTAGCAGTGGG 586  
DB 481 ACCAATGAGGCTGTGCTAGAGGTCACTGAGGATTTACGCACTAGCAGTGGG 540  
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DB 541 AAGATGAGGCTGTGCTAGAGGTCACTGAGGATTTACGCACTAGCAGTGGG 600  
QY 647 AAAATGCAAGCAAGTGTGTAGAGCTCAACCTGTACCTTAACGGAATTGACTACAGTA 706  
DB 601 AAAATGCAAGCAAGTGTGTAGAGCTCAACCTGTACCTTAACGGAATTGACTACAGTA 660  
QY 707 TTGGAGCAACAATCACTTCACTGCTTTAAACAAGCTGACTATTCAAGCACTTTACAT 766  
DB 661 TTGGAGCAACAATCACTTCACTGCTTTAAACAAGCTGACTATTCAAGCACTTTACAT 720  
QY 767 CTAGCTGTGGAATATGATTTACTTATTGACTAAGTTAGGTGAGGAACATCACTC 826  
DB 721 CTAGCTGTGGAATATGATTTACTTATTGACTAAGTTAGGTGAGGAACATCACTC 780  
QY 827 AGCTCATTAATCGGAGGCGCTTATCAACGGTAACTTATCTTATAGACTACAGACT 886  
DB 781 AGCTCATTAATCGGAGGCGCTTATCAACGGTAACTTATCTTATAGACTACAGACT 840  
QY 887 CAACTCTTGGGTATACAGTAATCTTACCTTCACTGCGGAACTTAAATATATGCGTCC 946  
DB 841 CAACTCTTGGGTATACAGTAATCTTACCTTCACTGCGGAACTTAAATATATGCGTCC 900  
QY 947 ACCTACTTGGAAACCTTATCCGTAAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCA 1006  
DB 901 ACCTACTTGGAAACCTTATCCGTAAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCA 960  
QY 1007 AAAAGGTGACAGAGTGGTCTGTGATAGAAAGCACTTGAACCTTACTATCTATAGAA 1066  
DB 961 AAAAGGTGACAGAGTGGTCTGTGATAGAAAGCACTTGAACCTTACTATCTATAGAA 1020  
QY 1067 ACTGACTTAGATTTATATTTGACAAAGATAGTAACGTTCCCTATGTCCCTGTATTTAT 1126  
DB 1021 ACTGACTTAGATTTATATTTGACAAAGATAGTAACGTTCCCTATGTCCCTGTATTTAT 1080  
QY 1127 TCCTGCTTGAACCGGCAATAGCTGCGCTGTATGTATCTAAAGACCGAAGCGCACTTACT 1186  
DB 1081 TCCTGCTTGAACCGGCAATAGCTGCGCTGTATGTATCTAAAGACCGAAGCGCACTTACT 1140  
QY 1187 ACACCATATGATCTATCAAAAGTTCACTATCGGCACTGCAAGATGACAACTATGTA 1246  
DB 1141 ACACCATATGATCTATCAAAAGTTCACTATCGGCACTGCAAGATGACAACTATGTA 1200  
QY 1247 TGTGTAAACCCCGGATATCATATCGCAAACTATGAGAAAGCGGTCTCTATATATAT 1306  
DB 1201 TGTGTAAACCCCGGATATCATATCGCAAACTATGAGAAAGCGGTCTCTATATATAT 1260  
QY 1307 AAACCAATCATGCAATGTTTATCTTATAGCGGGAATCTTAAAGCTCAGTGGGAATTC 1366  
DB 1261 AAACCAATCATGCAATGTTTATCTTATAGCGGGAATCTTAAAGCTCAGTGGGAATTC 1320  
QY 1367 GATGTAACTTATGAGAAATATCTCAATACAGATTTCTCAAGTATATATACAGGCAAT 1426  
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QY 1427 CTGATATCTCACTGAGCTTGGGAATGTCAACAACTGATCATGATCTTGAATAG 1486  
DB 1391 CTGATATCTCACTGAGCTTGGGAATGTCAACAACTGATCATGATCTTGAATAG 1440  
QY 1487 TTAGGAAAGCAACAGAAAACTAGCAAAAGTCAATGTCAACTGACTAGCACTGTCT 1546  
DB 1441 TTAGGAAAGCAACAGAAAACTAGCAAAAGTCAATGTCAACTGACTAGCACTGTCT 1500  
QY 1547 CTGATATCTCACTGATTTGATCATATCTCTGTTTGTGTATCTTACCTGAT 1606  
DB 1501 CTGATATCTCACTGATTTGATCATATCTCTGTTTGTGTATCTTACCTGAT 1560  
QY 1607 CTGATATCTCACTGATTTGATCAAGAAAGCGGCAACAAACCTTATTTGCTTGG 1666  
DB 1561 CTGATATCTCACTGATTTGATCAAGAAAGCGGCAACAAACCTTATTTGCTTGG 1620  
QY 1667 AATAATCTCACTGATTTGATGAGGCACTCAAAATGTGA 1708  
DB 1621 AATAATCTCACTGATTTGATGAGGCACTCAAAATGTGA 1662

RESULT 14  
US-08-804-372A-10  
; Sequence 10, Application US/08804372A  
; Patent No. 6183753  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Winslow, Barbara J.  
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,372A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 2552/39115E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1662 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1662  
; US-08-804-372A-10

Query Match 48.6%; Score 1631.6; DB 3; Length 1662;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTTATGATGCTGATCTATCCGGGTGGC 106  
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTTATGATGCTGATCTATCCGGGTGGC 60  
QY 107 CTGGCACTGAGTTCATCTGTCCGGCAAACTCCATTTGAGGAGGCGCTTTGAGCTGCA 166  
DB 61 CTGGTACTGAGTTCATCTGTCCGGCAAACTCCATTTGAGGAGGCGCTTTGAGCTGCA 120  
QY 167 GGAATTTGGTTAGAGAGCAAAAGCGTCAACATATATCACTGATCCAGACAGATCA 226  
DB 121 GGAATTTGGTTAGAGAGCAAAAGCAATATATCACTGATCCAGACAGATCA 180  
QY 227 ATCATAGTTAAAGCTCTCCGAAATCTGCCAAAGATTAAGAGCAATGTGGGAAGCCCC 286  
DB 181 ATCATAGTTAAAGCTCTCCGAAATCTGCCAAAGATTAAGAGCAATGTGGGAAGCCCC 240  
QY 287 TTGGATGCTATCAACAGAGCAATTTGACCACTTTGCTCAACCCCTTGGGATCTCATCCGT 346  
DB 241 TTGGATGCTATCAACAGAGCAATTTGACCACTTTGCTCAACCCCTTGGGATCTCATCCGT 300  
QY 347 AGGATCAAGAGCTCTGTGACTACATCTGAGGGGGAGACAGGGGGCGCTTATAGGCGC 406  
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QY 407 ATTAATGGCGGTGTGGCTCTTGGGGTTGCACTGCGCGCAAAATATACAGCGCGCGAGCT 466  
DB 361 ATTAATGGCGGTGTGGCTCTTGGGGTTGCACTGCGCGCAAAATATACAGCGCGCGAGCT 420  
QY 467 CTGATCAAGCGCAAAATATGCTGCGCAACATCTCCGCACTTAAGAGAGATTTGGCGCA 526  
DB 421 CTGATCAAGCGCAAAATATGCTGCGCAACATCTCCGCACTTAAGAGAGATTTGGCGCA 480  
QY 527 ACCAATGAGGCTGTGATGAGAGTCACTGACGGATTTATCGCAATGAGTGGAGTTGGG 586  
DB 481 ACCAATGAGGCTGTGATGAGAGTCACTGACGGATTTATCGCAATGAGTGGAGTTGGG 540  
QY 587 AAGATGAGCAGGTTTGTATATGACCAATTTAATAAACAAGCTCAGAAATTTAGACTGCATC 646  
DB 541 AAGATGAGCAGGTTTGTATATGACCAATTTAATAAACAAGCTCAGAAATTTAGACTGCATC 600  
QY 647 AAAATTCGACAGCAAGTTGGTGTAGAGTCAACCTGTAACTTAACCGAATTTGACATACGTA 706  
DB 601 AAAATTCGACAGCAAGTTGGTGTAGAGTCAACCTGTAACTTAACCGAATTTGACATACGTA 660  
QY 707 TTGGGACCAAAATCACTTCACTGCTTTAAACAAGCTGATATTTAGGCACTTTAACAT 766  
DB 661 TTGGGACCAAAATCACTTCACTGCTTTAAACAAGCTGATATTTAGGCACTTTAACAT 720  
QY 767 CTAGCTGTGAAATATGATTAATTTGATTTGAATTAAGTGTAGGGAACAATCAATCTC 826  
DB 721 CTAGCTGTGAAATATGATTAATTTGATTTGAATTAAGTGTAGGGAACAATCAATCTC 780  
QY 827 AGCTCATTAATCGGTAGCGGCTTAATCAACGGGTAACTTATCTATACGACTCAACACT 886  
DB 781 AGCTCATTAATCGGTAGCGGCTTAATCAACGGGTAACTTATCTATACGACTCAACACT 840  
QY 887 CAACCTTTGGGTATACAGGTAACTCTACCTTCACTGCGGGAACCTAATAATATGCTGCGC 946  
DB 841 CAACCTTTGGGTATACAGGTAACTCTACCTTCACTGCGGGAACCTAATAATATGCTGCGC 900  
QY 947 ACCTACTTGGAAACCTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCA 1006  
DB 901 ACCTACTTGGAAACCTTATCCGTAGACCAACAGGGGATTTGCTCGGCACTTGTCCCA 960  
QY 1007 AAAGTGTGACACAGGTGTGGTTCTGTGATTAAGAACTTGAACACTCATCTGTATAGAA 1066  
DB 961 AAAGTGTGACACAGGTGTGGTTCTGTGATTAAGAACTTGAACACTCATCTGTATAGAA 1020  
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DB 1021 ACTGACTTGAATTTATATTTGTACAGAAATAGTAAAGTTCCCTATGTCCTCGGTATTTAT 1080  
QY 1127 TCCTGCTTGAAGCGCAATACGTGCGCTGTATGTACTCAAGAACGGAAGGCGCACTTACT 1186

DB 1081 TCCTGCTTGAAGCGCAATACGTGCGCTGTATGTACTCAAGAACGGAAGGCGCACTTACT 1140  
QY 1187 ACACATATACATGACTATCAAAAGTTGAGTATGATGCTGCAATGCAAGATGACATGTAGA 1246  
DB 1141 ACACATATATGACTATCAAAAGTTGAGTATGATGCTGCAATGCAAGATGACATGTAGA 1200  
QY 1247 TGTGTAAACCCCGGGATTCATATGCGCAAACTATGAGAGAGCCGTGTCTTATATGAT 1306  
DB 1201 TGTGTAAACCCCGGGATTCATATGCGCAAACTATGAGAGAGCCGTGTCTTATATGAT 1260  
QY 1307 AAACAATCATGCAATGTTTATATCTTAAGGCGGATATACCTTAAGGCTCAGTGGGGAATTC 1366  
DB 1261 AAACAATCATGCAATGTTTATATCTTAAGGCGGATATACCTTAAGGCTCAGTGGGGAATTC 1320  
QY 1367 GATGTAACTTATGAGAAATATCTCAATGCAAGATTTCTCAATTAATATACAGGCAAT 1426  
DB 1321 GATGTAACTTATGAGAAATATCTCAATGCAAGATTTCTCAATTAATATACAGGCAAT 1380  
QY 1427 CTGTATATCTCAACAGCTTGGGAATGTCAACAACCTGATCAGTATATGCTTGAATAG 1486  
DB 1381 CTGTATATCTCAACAGCTTGGGAATGTCAACAACCTGATCAGTATATGCTTGAATAG 1440  
QY 1487 TTAGAGAAAGCAACGAAACCTAGCAAGTCAATGCTCAAGTCAATGCT 1546  
DB 1441 TTAGAGAAAGCAACGAAACCTAGCAAGTCAATGCTCAAGTCAATGCT 1500  
QY 1547 CTGATTAATCTATATGCTTTGACTATCATATCTCTTTTGGTATTAATTAATGCTGAT 1606  
DB 1501 CTGATTAATCTATATGCTTTGACTATCATATCTCTTTTGGTATTAATTAATGCTGAT 1560  
QY 1607 CTAGCATGCTACCTAATGTACAGCAAAAGCGCAACAAAACCTTATATGCTTGGG 1666  
DB 1561 CTAGCATGCTACCTAATGTACAGCAAAAGCGCAACAAAACCTTATATGCTTGGG 1620  
QY 1667 AATTAATCTTAATGATGAGAGGCACTTCAAAAATGTGA 1708  
DB 1621 AATTAATCTTAATGATGAGAGGCACTTCAAAAATGTGA 1662

RESULT 15  
PCT-US95-10245-12  
Sequence 12, Application PC/TUS9510245  
GENERAL INFORMATION:  
APPLICANT: SYNTRO CORPORATION  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10245  
FILING DATE: 09-AUG-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
TELEX: 422523  
INFORMATION FOR SRO ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1662 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
PCT-US95-10245-12

Query Match      48.6%; Score 1631.6; DB 6; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 47 ATGGGCTCCGAGACCTTGTACCAAGAACCCAGACCTTATGATGCTGACATCCGGGTGG 106
Db 1 ATGGGCTCCGAGACCTTGTACCAAGAACCCAGACCTTATGATGCTGACATCCGGGTGG 60

Qy 107 CTGGCAGTGAAGTTCATCTGTCCGGCAAACTCAATTGAGCAGGCTCTTGACAGTGA 166
Db 61 CTGGTACTGAAGTTCATCTGTCCGGCAAACTCAATTGAGCAGGCTCTTGACAGTGA 120

Qy 167 GGAATTGTGTTACAGAGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCA 226
Db 121 GGAATTGTGTTACAGAGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCA 180

Qy 227 ATCATATTAAAGCTCTCCCGAATCTGCCAAGATTAAGAGGATGTCGAAAGCCCC 286
Db 181 ATCATATTAAAGCTCTCCCGAATCTGCCAAGATTAAGAGGATGTCGAAAGCCCC 240

Qy 287 TTGGATGATTAACAAGAGACATTTGACCACTTGGCTCAACCCCTTGGTGTACTATCCGT 346
Db 241 TTGGATGATTAACAAGAGACATTTGACCACTTGGCTCAACCCCTTGGTGTACTATCCGT 300

Qy 347 AGGATTAACAAGAGCTGTGACTATCATCTGAGAGGAGGAGAGAGGAGGAGGAGGAGG 406
Db 301 AGGATTAACAAGAGCTGTGACTATCATCTGAGAGGAGGAGAGAGGAGGAGGAGGAGG 360

Qy 407 ATTATTTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATTAACAGCCGCGAGCT 466
Db 361 ATTATTTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATTAACAGCCGCGAGCT 420

Qy 467 CTGATTAACAAGGCAAAATATGTCGCAACATCTCCGACTTAAAGAGAGGATTCGCGCA 526
Db 421 CTGATTAACAAGGCAAAATATGTCGCAACATCTCCGACTTAAAGAGAGGATTCGCGCA 480

Qy 527 ACCAATGAGGCTGTGACTGAGAGTCACTGACGATTAATCGCAACTAGAGTGGAGTTGG 586
Db 481 ACCAATGAGGCTGTGACTGAGAGTCACTGACGATTAATCGCAACTAGAGTGGAGTTGG 540

Qy 587 AAGATGAGCAGGTTGTTATGACCAATTATTAATAACAGCTCAGAAATTGACTGCATC 646
Db 541 AAGATGAGCAGGTTGTTATGACCAATTATTAATAACAGCTCAGAAATTGACTGCATC 600

Qy 647 AAAATTGCAACGAGGTTGTGTAGAGCTCAACCTGTAACTTAACGGAATTGACTACAGTA 706
Db 601 AAAATTGCAACGAGGTTGTGTAGAGCTCAACCTGTAACTTAACGGAATTGACTACAGTA 660

Qy 707 TTCGAGACCAAAATCACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAT 766
Db 661 TTCGAGACCAAAATCACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAT 720

Qy 767 CTAGCTGTGGAATATGATTAATTAATGACTAAGTTAGGTGAGGAACTATCAATC 826
Db 721 CTAGCTGTGGAATATGATTAATTAATGACTAAGTTAGGTGAGGAACTATCAATC 780

Qy 827 AGCTCATTAATCGGTAGGCTTAATGACCGGTAACTTCTATAGACTCAAGACT 886
Db 781 AGCTCATTAATCGGTAGGCTTAATGACCGGTAACTTCTATAGACTCAAGACT 840

Qy 887 CAATCTTGGGTATACAGTAACTCTACCTTCAGTCGGGAACTAAATATATGCTGCC 946
Db 887 CAATCTTGGGTATACAGTAACTCTACCTTCAGTCGGGAACTAAATATATGCTGCC 900
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Db 841 CAATCTTGGGTATACAGTAACTCTACCTTCAGTCGGGAACTAAATATATGCTGCC 900
Qy 947 ACTTACTTGGAAACCTTATCCGTATAGCAACAACAGGGGATTTGCTCGCACTTGTCCA 1006
Db 901 ACTTACTTGGAAACCTTATCCGTATAGCAACAACAGGGGATTTGCTCGCACTTGTCCA 960
Qy 1007 AAAGTGTGACACAGTGGGTTCTGTGATAGAGAACTTGAACCTCATCTGTATAGA 1066
Db 961 AAAGTGTGACACAGTGGGTTCTGTGATAGAGAACTTGAACCTCATCTGTATAGA 1020
Qy 1067 ACTGACTTAAGTTTATATGTTGACAAAGAAATTAATAGTCCCTATGCTCCCTGATTTAT 1126
Db 1021 ACTGACTTAAGTTTATATGTTGACAAAGAAATTAATAGTCCCTATGCTCCCTGATTTAT 1080
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Db 1081 TCCTGCTTGAAGCGGCAATACCTCGGCTGTATGTATCTCAAGACGGAAGGCGCACTTACT 1140
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Db 1201 TGTGTTAAACCCCGGGTATATATGCGAAAACCTATGAGAAAGCCGTCTCTTAATAT 1260
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Db 1261 AAACATCATATGATTTTATCTTCTAGGCGGGAATCTTAAAGGCTCAGTGGGAAATTC 1320
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Db 1321 GATGTAACTTATCAGAAAGATATCTCAATATCAAGATTCAGTAAATATTAACAGGCAAT 1380
Qy 1427 CTGATATCTCACTGAGCTTGGGAATGTCAAACTCGATCAAGTAATGCTTTGAATAG 1486
Db 1381 CTGATATCTCACTGAGCTTGGGAATGTCAAACTCGATCAAGTAATGCTTTGAATAG 1440
Qy 1487 TTAGAGGAAGCAACAGAAACTAGCAAAAGTCAATGCTCAACTGACTAGACATCTGCT 1546
Db 1441 TTAGAGGAAGCAACAGAAACTAGCAAAAGTCAATGCTCAACTGACTAGACATCTGCT 1500
Qy 1547 CTCATTACTATATCTTTTGTGACTATCATATCTCTTGTTTTGTGATATCTTACCTGAT 1606
Db 1501 CTCATTACTATATCTTTTGTGACTATCATATCTCTTGTTTTGTGATATCTTACCTGAT 1560
Qy 1607 CTAGCATGTCTACTTAATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGG 1666
Db 1561 CTAGCATGTCTACTTAATGTACAGCAAAAGGCGCAACAAAACCTTATATGCTTGG 1620
Qy 1667 AATAATACTAGATCAGATGAGAGCACTTCAAAAATGTGA 1708
Db 1621 AATAATACTAGATCAGATGAGAGCACTTCAAAAATGTGA 1662
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Search completed: February 5, 2006, 02:50:00  
Job time : 577 secs



The Logo Bank (usps)



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QY	361	TGTGACTACATCTGGAGGGGGGAGACAGGGGGCGCTTAATGAGCGCATTTATGGCGGT	420
Dp	361	TGTGACTACATCTGGAGGGGGGAGACAGGGGGCGCTTAATGAGCGCATTTATGGCGGT	420
QY	421	GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCCGACGCTTGATACAAAGCAA	480
Dp	421	GGCTCTTGGGGTTGCAACTGCGGCAAAATTAACAGCGGCCGACGCTTGATACAAAGCAA	480
QY	481	ACAAAATGCTGCGCAACATCTTCCGACTTAAAGAGCATTTGCCGACAAACATGAGGCTGT	540
Dp	481	ACAAAATGCTGCGCAACATCTTCCGACTTAAAGAGCATTTGCCGACAAATGAGGCTGT	540
QY	541	GCATGAGGTCACTGACGGATTATGCAACTAGCACTGGCAGTGTGGGAAGATGACAGCTT	600
Dp	541	GCATGAGGTCACTGACGGATTATGCAACTAGCACTGGCAGTGTGGGAAGATGACAGCTT	600
QY	601	TGTTAATGACCAATTTAAATAAACAGCTCAGGAATTTAGACTGCATCAAAATTTGACACAGA	660
Dp	601	TGTTAATGACCAATTTAAATAAACAGCTCAGGAATTTAGACTGCATCAAAATTTGACACAGA	660
QY	661	AGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTTGACTACAGTATTTGCGACCAAAAT	720
Dp	661	AGTTGGTGTAGAGCTCAACCTGTACTTAACGGAATTTGACTACAGTATTTGCGACCAAAAT	720
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Dp	721	CACCTCACCTGCTTTAAACAAGCTGACTATTGAGGCACTTTAACAATCTAGCTGGGGAAA	780
QY	781	TATGAGATTACTTATTTAGTAAGTTAGGTGAGGAAACAATCAACTCAGCTCAATTAATCGG	840
Dp	781	TATGAGATTACTTATTTAGTAAGTTAGGTGAGGAAACAATCAACTCAGCTCAATTAATCGG	840
QY	841	TAGCGGCTTAATCACCGGTAAACCTTATCTATAGCACTCACAGACTCAACTCTTGGGTAAT	900
Dp	841	TAGCGGCTTAATCACCGGTAAACCTTATCTATAGCACTCACAGACTCAACTCTTGGGTAAT	900
QY	901	ACAGGTACTGACCTTCAAGTCGAGGGAACCTTAATTAATGAGTGCGACCTTCTTGGGAAC	960
Dp	901	ACAGGTACTGACCTTCAAGTCGAGGGAACCTTAATTAATGAGTGCGACCTTCTTGGGAAC	960
QY	961	CTTATCCGTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCAAAAGTGTGACACA	1020
Dp	961	CTTATCCGTAAGCAACAACAGGGGATTTGCTCGGCACTTGTCCAAAAGTGTGACACA	1020
QY	1021	GGTCGGTTCGTGTATAGGAAGACTTGACACCTCATACTGTATAGAACTGACTTAGATTT	1080
Dp	1021	GGTCGGTTCGTGTATAGGAAGACTTGACACCTCATACTGTATAGAACTGACTTAGATTT	1080
QY	1081	ATATTGTGCAAGAAATAGTAAGTCCCTATGTCCTCCCTGTAATTTATTCCTGCTGAGGG	1140
Dp	1081	ATATTGTGCAAGAAATAGTAAGTCCCTATGTCCTCCCTGTAATTTATTCCTGCTGAGGG	1140
QY	1141	CAATACGTGCGGCTGTATGTACTCAAAAGCGAAGCGGCACCTTACTACACCATACATATAC	1200
Dp	1141	CAATACGTGCGGCTGTATGTACTCAAAAGCGAAGCGGCACCTTACTACACCATACATATAC	1200
QY	1201	TATCAAAAGGTTCAGTCAATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCGCC	1260
Dp	1201	TATCAAAAGGTTCAGTCAATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCGCC	1260
QY	1261	GGGTATCATATCGCAAACTATGAGAAAGCGGTGTCTTAATAGTAAACATCATGCA	1320
Dp	1261	GGGTATCATATCGCAAACTATGAGAAAGCGGTGTCTTAATAGTAAACATCATGCA	1320
QY	1321	TGTTTATACCTTGAAGCGGGAATCACTTAAAGGTCAGTGGGGAATTCATGTAACTTATCA	1380
Dp	1321	TGTTTATACCTTGAAGCGGGAATCACTTAAAGGTCAGTGGGGAATTCATGTAACTTATCA	1380
QY	1381	GAAGAAATTCATACAAAGATTCCTCAAGTATATATAACAGGCATCTTGATATCTCAAC	1440

Db	1361	GAGGATATCTCAATACAAAGATTCTCAGATTAATTAATAAGGCAATCTTGATATCTCAAC	1440
Qy	1441	TGAGCTTGGGAATGTCACAACTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAACAA	1500
Db	1441	TGAGCTTGGGAATGTCACAACTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAACAA	1500
Qy	1501	CAGAAATCTAAGCAAAATCATATGTCMAACTGACATGACATCTCTCTCATTTACTTATAT	1560
Db	1501	CAGAAATCTAAGCAAAATCATATGTCMAACTGACATGACATCTCTCTCATTTACTTATAT	1560
Qy	1561	CGTTTGCATCTCATATCTCTGTTTTTGGTATCTTAGCCTGATTTCTAGCATGCTACT	1620
Db	1561	CGTTTGCATCTCATATCTCTGTTTTTGGTATCTTAGCCTGATTTCTAGCATGCTACT	1620
Qy	1621	AATGTACAGCAAAAGCGCAACAAAACCTTATATAGCCTTGGAAATAATTAATCTTAGA	1680
Db	1621	AATGTACAGCAAAAGCGCAACAAAACCTTATATAGCCTTGGAAATAATTAATCTTAGA	1680
Qy	1681	TCAGATGAGACCACTACAAAATATGTGACACAGATGAGACGAGTTTCCCTAATAG	1740
Db	1681	TCAGATGAGACCACTACAAAATATGTGACACAGATGAGACGAGTTTCCCTAATAG	1740
Qy	1741	TAAATTTGTTGTAAGTTCTGTGTAGCTGTCAAGTCAAGAGTTTAAAGAAAAAATCAACGGT	1800
Db	1741	TAAATTTGTTGTAAGTTCTGTGTAGCTGTCAAGTCAAGAGTTTAAAGAAAAAATCAACGGT	1800
Qy	1801	TGTAGATGACCAAGACGATATACGGGTAGAAACGGTAAAGAGACGCGCCCTCAATTGC	1860
Db	1801	TGTAGATGACCAAGACGATATACGGGTAGAAACGGTAAAGAGAGCGCGCCCTCAATTGC	1860
Qy	1861	GAGCCAGGCTTCACACCTCCGTTCTACCGCTTACCGACACAGTCTCTCAATATATGAC	1920
Db	1861	GAGCCAGGCTTCACACCTCCGTTCTACCGCTTACCGACACAGTCTCTCAATATATGAC	1920
Qy	1921	CGCGCGCTTACCAAGTTGGTTGAGATGATGAAAGAGAGCGCAAAAATATACATGGCGC	1980
Db	1921	CGCGCGCTTACCAAGTTGGTTGAGATGATGAAAGAGAGCGCAAAAATATACATGGCGC	1980
Qy	1981	TTGATATTTCCGGATTTGCATCTTATTTCTTAAACAGTAGTGAACCTTGGCTATATCTGAGCC	2040
Db	1981	TTGATATTTCCGGATTTGCATCTTATTTCTTAAACAGTAGTGAACCTTGGCTATATCTGAGCC	2040
Qy	2041	TCCTTTTATATAGCATAGGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG	2100
Db	2041	TCCTTTTATATAGCATAGGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG	2100
Qy	2101	ATTTCCAGGGCAGAAAGAAAGATTAACATCTACACTTGTGTTCCATTCAGATGTATGAT	2160
Db	2101	ATTTCCAGGGCAGAAAGAAAGATTAACATCTACACTTGTGTTCCATTCAGATGTATGAT	2160
Qy	2161	AGGATATTTAAGCAAGTGGCCCTTGAGTCTCCGTTGSCATTTGTTAAATACTGAGACACA	2220
Db	2161	AGGATATTTAAGCAAGTGGCCCTTGAGTCTCCGTTGSCATTTGTTAAATACTGAGACACA	2220
Qy	2221	ATTATGAACGCAATPAACATCTCTCTCTTATCAGATTAAATGAGCTGCAACACAGTGGG	2280
Db	2221	ATTATGAACGCAATPAACATCTCTCTCTTATCAGATTAAATGAGCTGCAACACAGTGGG	2280
Qy	2281	TGGGGGGGCACTATCCATGACCCAGATTTATATAGGGGGGATAGCCAAAGAACTCATTTGTA	2340
Db	2281	TGGGGGGGCACTATCCATGACCCAGATTTATATAGGGGGGATAGCCAAAGAACTCATTTGTA	2340
Qy	2341	GATGATGCTAGTATGTCACATCATCTCATCCCTGTCATTTCAAGAACATCTGAATTTT	2400
Db	2341	GATGATGCTAGTATGTCACATCATCTCATCCCTGTCATTTCAAGAACATCTGAATTTT	2400
Qy	2401	ATCCCGGCGCTTACTACAGATTCAGGTTGCACTCGAATACCCTCATTTTGACATGATGCT	2460
Db	2401	ATCCCGGCGCTTACTACAGATTCAGGTTGCACTCGAATACCCTCATTTTGACATGATGCT	2460
Qy	2461	ACCAATTATCTGTAACCCCATATATGTATATTTGTTGATGACAGATCACTCAATTTCA	2520
Db	2461	ACCAATTATCTGTAACCCCATATATGTATATTTGTTGATGACAGATCACTCAATTTCA	2520

Db 2461 ACCATTACTGCTACACCCATATGTATATTTGCTGTGATGACAGATCACTACATTCA 2520  
Qy 2521 TATCAGATTATTAAGCATTGGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Db 2521 TATCAGATTATTAAGCATTGGTGTGCTCCGACATCTGCAACAGGAGGATTTCTTTCT 2580  
Qy 2581 ACTCTGGTTCATCAACCTTGAGACACCCAAATGCGAAGTCTTGTGATGTGATGCA 2640  
Db 2581 ACTCTGGTTCATCAACCTTGAGACACCCAAATGCGAAGTCTTGTGATGTGATGCA 2640  
Qy 2641 ACTCCCGGGTGTGATGTGCTGTGCTCGAAGTCAACGAGACAGAGAGAAATTTAT 2700  
Db 2641 ACTCCCGGGTGTGATGTGCTGTGCTCGAAGTCAACGAGACAGAGAGAAATTTAT 2700  
Qy 2701 AACTCAGCTGTCCCTACGCGGATGTATCATGAGAGTTAGGGTTGACGCGCAGTACAC 2760  
Db 2701 AACTCAGCTGTCCCTACGCGGATGTATCATGAGAGTTAGGGTTGACGCGCAGTACAC 2760  
Qy 2761 GAAAGAGCCTAGATGTCAACATTTATCGGGGATGGGTGCGCACTACCCAGAGTA 2820  
Db 2761 GAAAGAGCCTAGATGTCAACATTTATCGGGGATGGGTGCGCACTACCCAGAGTA 2820  
Qy 2821 GGGGGTGGATCTTTATTTGACGCGGATGTGTTCTCAGTCTACGAGGGTTAAACCC 2880  
Db 2821 GGGGGTGGATCTTTATTTGACGCGGATGTGTTCTCAGTCTACGAGGGTTAAACCC 2880  
Qy 2881 AATTCAACCACTGACACTGTATCAGAGAGGAAATATGTATATCAAGCATATGATGAC 2940  
Db 2881 AATTCAACCACTGACACTGTATCAGAGAGGAAATATGTATATCAAGCATATGATGAC 2940  
Qy 2941 ACATGCCAGATGACAGACTACAGATTTGAAATGGCAAGTCTTGTATTAAGCTTGA 3000  
Db 2941 ACATGCCAGATGACAGACTACAGATTTGAAATGGCAAGTCTTGTATTAAGCTTGA 3000  
Qy 3001 CGGTTTGTGGGAAACCATATCAGACGCTATCTTATCTACAGGTCTCAACCTCTTA 3060  
Db 3001 CGGTTTGTGGGAAACCATATCAGACGCTATCTTATCTACAGGTCTCAACCTCTTA 3060  
Qy 3061 GGGGAAACCCGATCTGATCTGACCGCCCAACAGTCACTCATGCGGGCCGAGGC 3120  
Db 3061 GGGGAAACCCGATCTGATCTGACCGCCCAACAGTCACTCATGCGGGCCGAGGC 3120  
Qy 3121 AGAATTTCAACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180  
Db 3121 AGAATTTCAACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180  
Qy 3181 CCGCGCTTATTTATCTCTATGACAGTCAAGCAAAACAGCACTCTTCAATAGTCTTAT 3240  
Db 3181 CCGCGCTTATTTATCTCTATGACAGTCAAGCAAAACAGCACTCTTCAATAGTCTTAT 3240  
Qy 3241 ACATTCAGTCTTCACTCGGCGAGTATCTCCCTTGCCAGGCTTGCAAGAGTGCCT 3300  
Db 3241 ACATTCAGTCTTCACTCGGCGAGTATCTCCCTTGCCAGGCTTGCAAGAGTGCCT 3300  
Qy 3301 AACTCTGTGTCTTCTGAGTCTATACAGATCATTCCCTTAATCTTATATGAAC 3358  
Db 3301 AACTCTGTGTCTTCTGAGTCTATACAGATCATTCCCTTAATCTTATATGAAC 3358

RESULT 2  
US-09-741-744A-134  
; Sequence 134, Application US/09741744A  
; Publication No. US20030087417A1  
; GENERAL INFORMATION:  
; APPLICANT: Peeters, Bernadus  
; APPLICANT: de Leeuw, Olav  
; APPLICANT: Klaus, Guus  
; APPLICANT: Arnaud, Gielkens  
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnost  
; FILE REFERENCE: 2183-464US  
; CURRENT APPLICATION NUMBER: US/09/741, 744A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: PCT/NL99/00377

; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 134  
; LENGTH: 15186  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus labota  
US-09-741-744A-134  
Query Match 99.9%; Score 3353.2; DB 3; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ACGGTTGAGATTTCTGATTCGGGTTGGCGCCTTCCAGGTGCAAGATGGCTCCAGACC 60  
Db 4498 ACGGTTGAGATTTCTGATTCGGGTTGGCGCCTTCCAGGTGCAAGATGGCTCCAGACC 4557  
Qy 61 TTTCACCAAGAACCCAGACCTATGATGCTGATATCCGAGGTTGGCTGGAGCTGAGTTG 120  
Db 4558 TTTCACCAAGAACCCAGACCTATGATGCTGATATCCGAGGTTGGCTGGAGCTGAGTTG 4617  
Qy 121 CATCTGTCGGCAAACTCCATTGATGAGCAGGCTCTTTCAGCTGCAAGAAATGTGTATAC 180  
Db 4618 CATCTGTCGGCAAACTCCATTGATGAGCAGGCTCTTTCAGCTGCAAGAAATGTGTATAC 4677  
Qy 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCGACAGAGATCATATGTTAAGCT 240  
Db 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCGACAGAGATCATATGTTAAGCT 4737  
Qy 241 CTTCCGAAATCTGCGCAAGGTAAGAGGAGATGTCGCAAGGCCCCCTTGATGATACAA 300  
Db 4738 CTTCCGAAATCTGCGCAAGGTAAGAGGAGATGTCGCAAGGCCCCCTTGATGATACAA 4797  
Qy 301 CAGACATTTGACACTTTGTCTCAACCCCTTGTGATCTATCCGTATGATACAAAGTCT 360  
Db 4798 CAGACATTTGACACTTTGTCTCAACCCCTTGTGATCTATCCGTATGATACAAAGTCT 4857  
Qy 361 TGTGACTTACATCTGAGGAGGAGAGACAGGAGGCGCTTATAGGCGCATTTATGGCGTGT 420  
Db 4858 TGTGACTTACATCTGAGGAGGAGAGACAGGAGGCGCTTATAGGCGCATTTATGGCGTGT 4917  
Qy 421 GGCCTTGGGGTTGCACTGCGCGCAAAATTAACGCGCGCACTCTGATTAACAGCAA 480  
Db 4918 GGCCTTGGGGTTGCACTGCGCGCAAAATTAACGCGCGCACTCTGATTAACAGCAA 4977  
Qy 481 ACAAAATGTGCGCAACATCTCCGACTTAAAGAGAGATTCGCGCAACCAATGAGGCTGT 540  
Db 4978 ACAAAATGTGCGCAACATCTCCGACTTAAAGAGAGATTCGCGCAACCAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCACTGACGATTTATGCAATAGCAGTGGCAGTTGGGAAATGACAGACTT 600  
Db 5038 GCATGAGGTCACTGACGATTTATGCAATAGCAGTGGCAGTTGGGAAATGACAGACTT 5097  
Qy 601 TGTATATGACCAATTTATATAAACAAGCTCAGGAATTAAGCTGCATCAAAATTTGACAGCA 660  
Db 5098 TGTATATGACCAATTTATATAAACAAGCTCAGGAATTAAGCTGCATCAAAATTTGACAGCA 5157  
Qy 661 AGTTGTTGATGAGTCAACCGTATCTTAACGGAATTAAGCTCAGATTTGAGACCAAAAT 720  
Db 5158 AGTTGTTGATGAGTCAACCGTATCTTAACGGAATTAAGCTCAGATTTGAGACCAAAAT 5217  
Qy 721 CACTTCACTGCTTTAAACAAGCTGATTTACAGCACTTTTACATCTAGCTGTGTGAAA 780  
Db 5218 CACTTCACTGCTTTAAACAAGCTGATTTACAGCACTTTTACATCTAGCTGTGTGAAA 5277  
Qy 781 TATGATTTACTTATTTGACTAAGTTAGGTGAGGAAACATTAATCTCAGCTATTAATGCG 840  
Db 5278 TATGATTTACTTATTTGACTAAGTTAGGTGAGGAAACATTAATCTCAGCTATTAATGCG 5337  
Qy 841 TAGGCGCTTATCAACCGGTAACCTTATTTATGAGCTCAAGACTCAACTCTTGGGTAT 900  
Db 5338 TAGGCGCTTATCAACCGGTAACCTTATTTATGAGCTCAAGACTCAACTCTTGGGTAT 5397

QY 901 ACAGGTACTCTACCTTCAGTCGGGAACTTAAATATGCGGCCACTTCTTGAAC 960  
DB 5398 ACAGGTAACTCTACCTTCAGTCGGGAACTTAAATATGCGGCCACTTCTTGAAC 5457  
QY 961 CTTATCCGTAGCAACAACGGGGATTGGCTCGGCACTTGTCCCAAAAGTGAGACA 1020  
DB 5458 CTTATCCGTAGCAACAACGGGGATTGGCTCGGCACTTGTCCCAAAAGTGAGACA 5517  
QY 1021 GGTGCGTCTGTGTATAGAACTTGAACCTCATCTGTATAGAAACTGACTTGAATT 1080  
DB 5518 GGTGCGTCTGTGTATAGAACTTGAACCTCATCTGTATAGAAACTGACTTGAATT 5577  
QY 1081 ATATTGTACAAGATAGTAACCTTCCCTATGTCCCTGGTATTTTATTCCTGCTTGAACGG 1140  
DB 5578 ATATTGTACAAGATAGTAACCTTCCCTATGTCCCTGGTATTTTATTCCTGCTTGAACGG 5637  
QY 1141 CATACGTCGGCCGTGTATCTCAAAAGACCGAAGGGGCACTTACTACACATACATGAC 1200  
DB 5638 CATACGTCGGCCGTGTATCTCAAAAGACCGAAGGGGCACTTACTACACATACATGAC 5697  
QY 1201 TATCAAGGTTCACTCATCCGCACTGCAAGATGACAACATGTATGTGTAAACCCGCC 1260  
DB 5698 TATCAAGGTTCACTCATCCGCACTGCAAGATGACAACATGTATGTGTAAACCCGCC 5757  
QY 1261 GGGTATCATATCCGAAACTATGAGAAAGCCGTGTCTCTAATATAGATAACATCATGCA 1320  
DB 5758 GGGTATCATATCCGAAACTATGAGAAAGCCGTGTCTCTAATATAGATAACATCATGCA 5817  
QY 1321 TGTTTATCTTGTAGCGGGATTACTTAAAGCTCAGTGGGAAATTCATGTAACTTATCA 1380  
DB 5818 TGTTTATCTTGTAGCGGGATTACTTAAAGCTCAGTGGGAAATTCATGTAACTTATCA 5877  
QY 1381 GAAGAATATCTCAATATACAAGATTCTCAAGTAAATATATACAGCAATCTTGTATCTCAAC 1440  
DB 5878 GAAGAATATCTCAATATACAAGATTCTCAAGTAAATATATACAGCAATCTTGTATCTCAAC 5937  
QY 1441 TGAGCTTGGAAATGTCAACAATCTGATCAGTATGCTTGTATATAGTTAGAGAAACAA 1500  
DB 5938 TGAGCTTGGAAATGTCAACAATCTGATCAGTATGCTTGTATATAGTTAGAGAAACAA 5997  
QY 1501 CAGAAAACCTAGCAAAAGTCAATGTCAACCTGACAGTCAACATCTGCTCTCATTAATCTAT 1560  
DB 5998 CAGAAAACCTAGCAAAAGTCAATGTCAACCTGACAGTCAACATCTGCTCTCATTAATCTAT 6057  
QY 1561 CGTTTGTACTATCATCTCTGTTTGTGTACTTACCTAGCTGATCTTACGATCTTACT 1620  
DB 6058 CGTTTGTACTATCATCTCTGTTTGTGTACTTACCTAGCTGATCTTACGATCTTACT 6117  
QY 1621 AATGTACAGCAAAAGGCGCAACAAACCTTATATGCTTGGAAATATCTTAGA 1680  
DB 6118 AATGTACAGCAAAAGGCGCAACAAACCTTATATGCTTGGAAATATCTTAGA 6177  
QY 1681 TCGATGAGAGCCACTTACAAAATGTGAACACAGATGAGAAAGCAAGTTTCCCTATAG 1740  
DB 6178 TCGATGAGAGCCACTTACAAAATGTGAACACAGATGAGAAAGCAAGTTTCCCTATAG 6237  
QY 1741 TAATTTGTGGAAGTCTGTAGTCTGTCAATTCAGAGTTTAAAGAAAACCTAACCGGT 1800  
DB 6238 TAATTTGTGGAAGTCTGTAGTCTGTCAATTCAGAGTTTAAAGAAAACCTAACCGGT 6297  
QY 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTTCATATTGC 1860  
DB 6298 TGTAGATGACCAAGAGAGAGATATACGGGTAGAACGTTAAGAGAGCCGCCCTTCATATTGC 6357  
QY 1861 GAGCCAGGCTTCAACAATCTCGTTCTTACCGCTTCAACGACACAGTCTCTCATATGAGAC 1920  
DB 6358 GAGCCAGGCTTCAACAATCTCGTTCTTACCGCTTCAACGACACAGTCTCTCATATGAGAC 6417  
QY 1921 CGGCGCGTTAGCAAGTTGGCTTATAGAAATGATGAAAGAGAGAAAATATACATGCGC 1980  
DB 6418 CGGCGCGTTAGCAAGTTGGCTTATAGAAATGATGAAAGAGAGAAAATATACATGCGC 6477  
QY 1981 TTGATATTCGGAGTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 2040

DB 6478 TTGATATTCGGAGTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGTAGCC 6537  
QY 2041 TCCCTTTTATATAGCATGCGGGCTAGACACCTAGCCATCTTGTAGCATACCGACTAGG 2100  
DB 6538 TCCCTTTTATATAGCATGCGGGCTAGACACCTAGCCATCTTGTAGCATACCGACTAGG 6597  
QY 2101 ATTTCCAGGGCAGAGAAAAGATTACATCTTACACTTGTGTTCCATATCAAGATGTATGAT 2160  
DB 6598 ATTTCCAGGGCAGAGAAAAGATTACATCTTACACTTGTGTTCCATATCAAGATGTATGAT 6657  
QY 2161 AGGATATATAGCAAGTGGCCCTTGTAGTCCGTTGGCACTTGTAAATATCTGAGACCA 2220  
DB 6658 AGGATATATAGCAAGTGGCCCTTGTAGTCCGTTGGCACTTGTAAATATCTGAGACCA 6717  
QY 2221 ATTTAGAACCAATTAACATCTCTCTTATCAGTTAATGAGCTGCAACACAGTGGG 2280  
DB 6718 ATTTAGAACCAATTAACATCTCTCTTATCAGATTATGAGCTGCAACACAGTGGG 6777  
QY 2281 TGGGGGGCACTTATCCATGACCAAGATTATAGGGGGATAGGCCAAAGAACTCATTTGTA 2340  
DB 6778 TGGGGGGCACTTATCCATGACCAAGATTATAGGGGGATAGGCCAAAGAACTCATTTGTA 6837  
QY 2341 GATATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
DB 6838 GATATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6897  
QY 2401 ATCCGGCGCCTTACTACAGGATCAGGTTGCACTGCAATACCTCATTTGACATGAGTGT 2460  
DB 6898 ATCCGGCGCCTTACTACAGGATCAGGTTGCACTGCAATACCTCATTTGACATGAGTGT 6957  
QY 2461 ACCCATTAATGCTACACCCCAATTAATGTAATGTTGTCTGATGACAGAGATCTACATTTCA 2520  
DB 6958 ACCCATTAATGCTACACCCCAATTAATGTAATGTTGTCTGATGACAGAGATCTACATTTCA 7017  
QY 2521 TATCAGATTTTACACTTGGTGTGCTCCGGACATCTGGCAACAGGAGGATTTCTTCT 2580  
DB 7018 TATCAGATTTTACACTTGGTGTGCTCCGGACATCTGGCAACAGGAGGATTTCTTCT 7077  
QY 2581 ACTCTGGGTTCCATCAACCTGAGACGACACCAAAATGGAAGTCTTGCAGTGTGAGTGA 2640  
DB 7078 ACTCTGGGTTCCATCAACCTGAGACGACACCAAAATGGAAGTCTTGCAGTGTGAGTGA 7137  
QY 2641 ACTCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAT 2700  
DB 7138 ACTCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAT 7197  
QY 2701 AACTCAGCTGTCCCTACGCGGATGTACATGAGGAGTTAGGTTCCAGCGGCCAGTATCAC 2760  
DB 7198 AACTCAGCTGTCCCTACGCGGATGTACATGAGGAGTTAGGTTCCAGCGGCCAGTATCAC 7257  
QY 2761 GAAAAGGACCTAGATGTCAACAATTAATGAGGGAATGGGTGGCCAACTCCAGAGATA 2820  
DB 7258 GAAAAGGACCTAGATGTCAACAATTAATGAGGGAATGGGTGGCCAACTCCAGAGATA 7317  
QY 2821 GGGGGTGTGATCTTTTATATGACAGCCGCGTATGCTTCACTTACGAGGGTTAAAAACC 2880  
DB 7318 GGGGGTGTGATCTTTTATATGACAGCCGCGTATGCTTCACTTACGAGGGTTAAAAACC 7377  
QY 2881 AATTTCACCAAGTACACTGTACAGAAAGGAAATATGTGATATACAGCAATACATGAC 2940  
DB 7378 AATTTCACCAAGTACACTGTACAGAAAGGAAATATGTGATATACAGCAATACATGAC 7437  
QY 2941 ACATGCCCAATAGAGCAAGACTACCAATTCGAATGGCCAAAGTCTTGTAATAGCCCTGGA 3000  
DB 7438 ACATGCCCAATAGAGCAAGACTACCAAGTTCGAATGGCCAAAGTCTTGTAATAGCCCTGGA 7497  
QY 3001 CGGTTTGTGAGAAAGCATACAGAGGCTATCTTATCTTATCAAGGTGTCAATCTCTTA 3060  
DB 7498 CGGTTTGTGAGAAAGCATACAGAGGCTATCTTATCTTATCAAGGTGTCAATCTCTTA 7557  
QY 3061 GAGCAAGACCCGGTACTGACTGTATCCGCCCAACAGTCACTCATGCGGGCCGAAAGCC 3120

Db 7558 GGGAGAACCCGGTACTGACTGTACCCGCAACAGTACACTCATGGGGCCGAAGGC 7617  
Qy 3121 AGAATTCACAGTAGGAGACTCATTTCTTGATCAAGGGGTATCATCTTCTCT 3180  
Db 7618 AGAATTCACAGTAGGAGACTCATTTCTTGATCAAGGGGTATCATCTTCTCT 7677  
Qy 3181 CCGCGCTTATTAATCTTATGACAGTACAGCAAAACAGCCACTTTCATATGCTTAT 3240  
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Qy 3241 ACATTCAGTCTTCACTCGCGCCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC 3300  
Db 7738 ACATTCAGTCTTCACTCGCGCCAGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC 7797  
Qy 3301 AACTCGTGTACTGAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358  
Db 7798 AACTCGTGTACTGAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

## RESULT 3

US-10-377-718-3  
; Sequence 3, Application US/10377718  
; Publication No. US20030175291A1  
; GENERAL INFORMATION:  
; APPLICANT: KUD, Tsun Yuang  
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO  
; FILE REFERENCE: 39734-186920  
; CURRENT APPLICATION NUMBER: US/10/377, 718  
; CURRENT FILING DATE: 2003-03-04  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 15186  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus (NDV)  
US-10-377-718-3

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTGAAGATTCTGATCCCGGTTGGCGCCCTTCAGAGTGAAGATGGGCTCCAGACC 60  
Db 4498 ACGGGTGAAGATTCTGATCCCGGTTGGCGCCCTTCAGAGTGAAGATGGGCTCCAGACC 4557  
Qy 61 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCCGGGTTGCCCTGGACCTGAGTTG 120  
Db 4558 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCCGGGTTGCCCTGGACCTGAGTTG 4617  
Qy 121 CATCTGCGGCAAACTCCATGTATGGAGGCTCTTGACAGCTGCAAGAAATTTGGTTAC 180  
Db 4618 CATCTGCGGCAAACTCCATGTATGGAGGCTCTTGACAGCTGCAAGAAATTTGGTTAC 4677  
Qy 181 AGAGAACAAAGCCGCTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240  
Db 4678 AGAGAACAAAGCCGCTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737  
Qy 241 CCTTCGCAATCTGCCCAAGATAGAGGCAATGTCGAAAGCCCTTGGATGCAATCAA 300  
Db 4738 CCTTCGCAATCTGCCCAAGATAGAGGCAATGTCGAAAGCCCTTGGATGCAATCAA 4797  
Qy 301 CAGGACATTGACCACTTTGCTCACCCCTTGATGACTCTATCCGTAGATACAAAGATC 360  
Db 4798 CAGGACATTGACCACTTTGCTCACCCCTTGATGACTCTATCCGTAGATACAAAGATC 4857  
Qy 361 TGTGACTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCCATTAATTTGGCGGTGT 420  
Db 4858 TGTGACTACATCTGAGGGGGAGACAGGGGCGCTTATAGCGCCATTAATTTGGCGGTGT 4917  
Qy 421 GGGCTTTGGGGTTGCACTGCGCGCAAAATACAGCGGCGGACGCTTGATACAGCCAA 480  
Db 4918 GGGCTTTGGGGTTGCACTGCGCGCAAAATACAGCGGCGGACGCTTGATACAGCCAA 4977

Qy 481 ACAAATGCTGCCAATCTCTCCGACTTAAAGAGACATGGCCGCAACCAATGAGGCTGT 540  
Db 4978 ACAAATGCTGCCAATCTCTCCGACTTAAAGAGACATGGCCGCAACCAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCACTGACGGATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 600  
Db 5038 GCATGAGGTCACTGACGGATTAATGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT 5097  
Qy 601 TGTTAATGACCAATTTAATAAACAAGTCAAGAAATTAAGTGCATCAAAATTTGACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATAAACAAGTCAAGAAATTAAGTGCATCAAAATTTGACAGCA 5157  
Qy 661 AGTTGGTGTAGAGTCAACCTGTACTTAACCGAATTAAGTCAAGTATTTGGACCAAAAT 720  
Db 5158 AGTTGGTGTAGAGTCAACCTGTACTTAACCGAATTAAGTCAAGTATTTGGACCAAAAT 5217  
Qy 721 CACTTACCGCTTTAAACAAGTGAATTAATTCAGGCACTTAACTAATGAGTGTGAAA 780  
Db 5218 CACTTACCGCTTTAAACAAGTGAATTAATTCAGGCACTTAACTAATGAGTGTGAAA 5277  
Qy 781 TATGATTAATCTTAATTAAGTGAAGTGAAGGAAACAATCAACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATCTTAATTAAGTGAAGTGAAGGAAACAATCAACTCAGCTCATTAATCGG 5337  
Qy 841 TAGCGGCTTAATCAACCGGTAACTCTTAATACACTCACAGACTCAACTCTTGGGTAT 900  
Db 5338 TAGCGGCTTAATCAACCGGTAACTCTTAATACACTCACAGACTCAACTCTTGGGTAT 5397  
Qy 901 ACAGGTAACTCTAATCTTCACTGAGGGAACCTAAATTAATGCTGCGCACTTGGAAAC 960  
Db 5398 ACAGGTAACTCTAATCTTCACTGAGGGAACCTAAATTAATGCTGCGCACTTGGAAAC 5457  
Qy 961 CTTATCCGTGAAGCAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 5458 CTTATCCGTGAAGCAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCTTCTGTGTATAGAAAGAACTTGAACCTCATCTATGTAGAAACTGACTTAATTT 1080  
Db 5518 GGTGCTTCTGTGTATAGAAAGAACTTGAACCTCATCTATGTAGAAACTGACTTAATTT 5577  
Qy 1081 ATATTGTGAAGAAATTAATTAATCTTCTTATGTCCTTGGTATTAATCTTCTGAGCGG 1140  
Db 5578 ATATTGTGAAGAAATTAATTAATCTTCTTATGTCCTTGGTATTAATCTTCTGAGCGG 5637  
Qy 1141 CAATACGTCGCGCTGTATGTACTCAAGAAGGCGCACTTACTACACATACATGAC 1200  
Db 5638 CAATACGTCGCGCTGTATGTACTCAAGAAGGCGCACTTACTACACATACATGAC 5697  
Qy 1201 TATCAAAAGTTCAAGTCACTGCAACCTGCAAGATGACAAATGTAGATGTGTAACCCGCC 1260  
Db 5698 TATCAAAAGTTCAAGTCACTGCAACCTGCAAGATGACAAATGTAGATGTGTAACCCGCC 5757  
Qy 1261 GGGTATCATATCGCAAAACTATGAGAAAGCCGTCTCTTAATAGATTAACAAATGATCAA 1320  
Db 5758 GGGTATCATATCGCAAAACTATGAGAAAGCCGTCTCTTAATAGATTAACAAATGATCAA 5817  
Qy 1321 TGTTTTATCCTTAGGCGGGAATTAATTAAAGGCTCAGTGGGGAATTCGATGTAACTTAATCA 1380  
Db 5818 TGTTTTATCCTTAGGCGGGAATTAATTAAAGGCTCAGTGGGGAATTCGATGTAACTTAATCA 5877  
Qy 1381 GAAGAAATATCTCAATACAAATTTCTCAAGTAATTAATTAACAGGCAATCTTGAATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATACAAATTTCTCAAGTAATTAATTAACAGGCAATCTTGAATCTCAAC 5937  
Qy 1441 TGAAGTTGGGAATGTCAACAATCTGATCAAGTAATGCTTTGAATTAAGTTAAGGAACAA 1500  
Db 5938 TGAAGTTGGGAATGTCAACAATCTGATCAAGTAATGCTTTGAATTAAGTTAAGGAACAA 5997  
Qy 1501 CAGAAACTGAGCAAAAGTCAATGCAACCTGACATGACAGCAATCTGCTCATTAACCTAAT 1560  
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Qy 1561 CGTTTGACTATCATATCTCTGTTTGTGTATTAATGACCTGATTTCTAGACATGCTAAT 1620

Db 6058 CGTTTACTATCATCTCTGTTTGTGTAATGCTGATTCAGATCTACCT 6117  
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 Db 6118 AATGTACAGCAAAAGGCGCAACAAAACCTTATTAATGCTTGGGAATATATCTAGA 6177  
 Qy 1681 TCAGATGAGAGCCCTACAAAATGTGAAACAGATGAGAGAGAGAGTTTCCCTAATAG 1740  
 Db 6178 TCAGATGAGAGCCCTACAAAATGTGAAACAGATGAGAGAGAGAGTTTCCCTAATAG 6237  
 Qy 1741 TAATTTGTGAAAGTTCTGTACTGTCTGATTCAGAGATTGAAGAAAACCTACCGGT 1800  
 Db 6238 TAATTTGTGAAAGTTCTGTACTGTCTGATTCAGAGATTGAAGAAAACCTACCGGT 6297  
 Qy 1801 TGTAGATGACCAAGAGAGATATACGGGTAGAGCGGTAAAGAGAGCGCCCTCAATTCG 1860  
 Db 6298 TGTAGATGACCAAGAGAGATATACGGGTAGAGCGGTAAAGAGAGCGCCCTCAATTCG 6357  
 Qy 1861 GAGCAGAGCTTACAACTCCGTTCTACCGCTTACCGACAAAGTCTCAATCATGAGAC 1920  
 Db 6358 GAGCAGAGCTTACAACTCCGTTCTACCGCTTACCGACAAAGTCTCAATCATGAGAC 6417  
 Qy 1921 CGGCGCTTACCGCAAGTTGGCTTAGAGATGATGAAAAGAGGCAAAAATACATGGCGC 1980  
 Db 6418 CGGCGCTTACCGCAAGTTGGCTTAGAGATGATGAAAAGAGGCAAAAATACATGGCGC 6477  
 Qy 1981 TTGATATTCGGATTTGCAATCTTATCTTAAACAGTATGATCCTTGGCTATCTGAGCC 2040  
 Db 6478 TTGATATTCGGATTTGCAATCTTATCTTAAACAGTATGATCCTTGGCTATCTGAGCC 6537  
 Qy 2041 TCCCTTTATATAGCATGGGGCTAGACACATGAGCATCTTGTAGGCATACCGATAGG 2100  
 Db 6538 TCCCTTTATATAGCATGGGGCTAGACACATGAGCATCTTGTAGGCATACCGATAGG 6597  
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 Db 6838 GATGATGCTATGATGTCATCATCTTCCATCCCTGATTTCAAGAACTATGAAATTTT 6897  
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 Qy 2581 ACTCTGGCTTCAATCAACTGACGACACCAAAATGGAAGTCTTCAAGTGTAGTGA 2640  
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 Qy 2641 ACTCCCTGGGTTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTAT 2700

Db 7138 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAACGAGACAGAGAAAGATTAT 7197  
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 Db 7198 AACTCAGCTGTCCCTTACGCGAGATGATCATGAGAGTTAGGGTTGACGCGCACTACAC 7257  
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 Db 7258 GAAAGAGCTTATATGTCACAACTTATTTGGGGAATGCGGTGGCACTACCCGAGATA 7317  
 Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGCGTATGTTCTCACTTACGAGGGTTAAACCC 2880  
 Db 7318 GGGGGTGGATCTTTTATTTGACAGCGCGCTATGTTCTCACTTACGAGGGTTAAACCC 7377  
 Qy 2881 AATTCCACCAAGTACACTGTACAGAAAGGAAATATGATATATCAACGATACATGAC 2940  
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 Qy 2941 ACATGCCAGATGACAAAGTACAGATTCGAATGGCCAAAGTTTGTATTAAGCTTGA 3000  
 Db 7438 ACATGCCAGATGACAAAGTACAGATTCGAATGGCCAAAGTTTGTATTAAGCTTGA 7497  
 Qy 3001 CGGTTTGTGGGAAAGCATACAGAGAGCTATCTTATCTATCAAGTGTCAACATCTTA 3060  
 Db 7498 CGGTTTGTGGGAAAGCATACAGAGAGCTATCTTATCTATCAAGTGTCAACATCTTA 7557  
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 Db 7558 GCGGAAAGCCGGTACTGATGATCCGCCCAACAGTCAACTCATGAGGGGCCGAAAGC 7617  
 Qy 3121 AGAATTTTCAAGTAGGGAATCTCATTTTCTGTATTAAGAGGATCATATCTTCT 3180  
 Db 7618 AGAATTTTCAAGTAGGGAATCTCATTTTCTGTATTAAGAGGATCATATCTTCT 7677  
 Qy 3181 CCGCGTTATTTATCTTATCTTATGACAGTACAGCAACAAACAGCACTCTTCAATGCTTAT 3240  
 Db 7678 CCGCGTTATTTATCTTATCTTATGACAGTACAGCAACAAACAGCACTCTTCAATGCTTAT 7737  
 Qy 3241 ACATTCATGCTTCACTCGGCGAGATGATCTCTTCCAGAGCTTACAGAAAGTGGCCC 3300  
 Db 7738 ACATTCATGCTTCACTCGGCGAGATGATCTCTTCCAGAGCTTACAGAAAGTGGCCC 7797  
 Qy 3301 AACTCGTGTGTAATGAGTCTTATACAGATTCATATCCCTAATCTTCTATAGAAAC 3358  
 Db 7798 AACTCGTGTGTAATGAGTCTTATACAGATTCATATCCCTAATCTTCTATAGAAAC 7855

RESULT 4  
 US-10-429-735-3  
 / Sequence 3, Application US/10429735  
 / Publication No. US20030207836A1  
 / GENERAL INFORMATION:  
 / APPLICANT: KDO, Tsun Yuang  
 / TITLE OF INVENTION: VACCINE ACCELERATOR FACTOR (VAF) FOR IMPROVEMENT OF VACCINATIONS  
 / FILE REFERENCE: 39734-188449  
 / CURRENT APPLICATION NUMBER: US/10/429, 735  
 / CURRENT FILING DATE: 2003-05-06  
 / NUMBER OF SEQ ID NOS: 19  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 3  
 / LENGTH: 15186  
 / TYPE: DNA  
 / ORGANISM: Newcastle disease virus (NDV)  
 US-10-429-735-3

Query Match 99.9%; Score 3353.2; DB 6; Length 15186;  
 Best Local Similarity 99.9%; Pired. No. 0;  
 Matches 3353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGTRGAGAGATTTCGATCCCGGTTGGGCGCTCCAGGTGCAAGTGGGCTCCAGACC 60  
 Db 4498 ACGGTRGAGAGATTTCGATCCCGGTTGGGCGCTCCAGGTGCAAGTGGGCTCCAGACC 4557



Qy 61 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCGGGTTGCGCTGGCACTGAATTG 120  
Db 4558 TTCTACCAAGAACCCAGACCTTATGATGCTGACTATCGGGTTGCGCTGGCACTGAATTG 4617  
Qy 121 CATCTGTCCGGCAAACTTCATTTGATGGAGGCTCTTGGCACTGAGAAATTGGTTAC 180  
Db 4618 CATCTGTCCGGCAAACTTCATTTGATGGAGGCTCTTGGCACTGAGAAATTGGTTAC 4677  
Qy 181 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGAAATCAATGATTAAGCT 240  
Db 4678 AGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGAAATCAATGATTAAGCT 4737  
Qy 241 CCTCCCAATCTGCCCAGAAAGATAGAGAGGCACTGTGCAAAAGCCCTTGGATGATCAAA 300  
Db 4738 CCTCCCAATCTGCCCAGAAAGATAGAGAGGCACTGTGCAAAAGCCCTTGGATGATCAAA 4797  
Qy 301 CAGGACATTTGACCACTTTGCTACCCCTTGGTGAATCTTATCCGTAGGATACAAAGATC 360  
Db 4798 CAGGACATTTGACCACTTTGCTACCCCTTGGTGAATCTTATCCGTAGGATACAAAGATC 4857  
Qy 361 TGTGATCTACATCTGAGAGGGGGAGACAGGGGCGCTTATAGCGCATTAATTGGCGGTGT 420  
Db 4858 TGTGATCTACATCTGAGAGGGGGAGACAGGGGCGCTTATAGCGCATTAATTGGCGGTGT 4917  
Qy 421 GGCTCTTGGGGTTGCAACTGCGGCAAAATACAGCGGCGCAAGCTCTGATACAAAGCCAA 480  
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Qy 481 ACAAAATGCTGCCAATCATCTCCGACTTTAAAGAGACATTTGCCGCAATGAGGCTGT 540  
Db 4978 ACAAAATGCTGCCAATCATCTCCGACTTTAAAGAGACATTTGCCGCAATGAGGCTGT 5037  
Qy 541 GCATGAGGTCACTAGCGGATATGCGCACTAGAGTGGCAATGGGAGATGACAGAGTT 600  
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Qy 781 TATGATTAATCTTATTTGACTAAGTTAGGTAGGGAAACATCAACTCAGCTCATTAATCGG 840  
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Db 5578 ATATTGTACAAAGATAGTAAGTTCCCTATATGTCCTTGGTATTTATTCCTGTTAGAGGG 5637

Qy 1141 CAATACGTCGGCCTGTATGTACTCAAGAACCGAAGGCGCACTTACTACACCATATGAC 1200  
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Qy 1261 GGGTATCATATCGCAAACTATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCA 1320  
Db 5758 GGGTATCATATCGCAAACTATGAGAAAGCCGTCTCTTAATAGATAAACAATCATGCA 5817  
Qy 1321 TGTTTATCTTTAGCGGGGATTAATTTAAGCTCAGTGGGAAATTCATGATTAATCA 1380  
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Qy 1381 GAAGATATCTCAATPACAAAGTTCTCAAGTATATATAAGCAATCTTGATATCTCAAC 1440  
Db 5878 GAAGATATCTCAATPACAAAGTTCTCAAGTATATATAAGCAATCTTGATATCTCAAC 5937  
Qy 1441 TGAGCTTGGGAATGTCAACATCGATCAATGATGCTTGAATATAGTAAAGCA 1500  
Db 5938 TGAGCTTGGGAATGTCAACATCGATCAATGATGCTTGAATATAGTAAAGCA 5997  
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Db 5998 CAGAAACTAGACAAAGTCAATGTCAAACTGACATGACATCTGCTCTCATTAATAT 6057  
Qy 1561 CGTTTGAATCATCATCTCTGTTTGTATGATCTTGAAGCTTCTAGCATGCTACT 1620  
Db 6058 CGTTTGAATCATCATCTCTGTTTGTATGATCTTGAAGCTTCTAGCATGCTACT 6117  
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Db 6358 GAGCGAGCTTCAACAACCTCGTTCTACCGCTTCAACGACAAACAGTCTCAATCATGAC 6417  
Qy 1921 CGCGCGCTTACCAAGTTGCTGTAGAAATGATGAAAGAGGCGAAAAATACATGAGGCG 1980  
Db 6418 CGCGCGCTTACCAAGTTGCTGTAGAAATGATGAAAGAGGCGAAAAATACATGAGGCG 6477  
Qy 1981 TTGATATTCGGGAATTTGCAATCTTATCTTAAACAGTATGACTTGGCTATATCTGTAGCC 2040  
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Qy 2341 GATGATGCTAGTGTACATCATCTTCTCTGATTTTCAAGAACATCTGAATTTT 2400  
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Qy 2401 ATCCCGGCGCTTACTAAGATTCAGTGTGCACTGGAAATACCCCTAATTGACATAGTGT 2460  
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Qy 2461 ACCCATTAATGCTTACACCCATATGTAATATTTGTCTGATTCAGAGATTCATCTCATTTCA 2520  
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Qy 2521 TATCAGATTATTAAGCACTTGTGTGCTCCGACATCTGCAACAGGGAGGTAATCTTTTCT 2580  
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Qy 2641 ACTCCCGGTTGTGATGTCTGTGCTCGAAAGTTCACGAGACAGAGAAAGATTTAT 2700  
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Qy 2821 GGGGGTGGATCTTTTATTTGACAGCGGCTATGTTCTCAGTCTACGAGGGTTAAACC 2880  
Db 7318 GGGGGTGGATCTTTTATTTGACAGCGGCTATGTTCTCAGTCTACGAGGGTTAAACC 7377  
Qy 2881 AATTCAACCAAGTACCTGTATCAGAAAGGAAATATGTATATCAAGCATAATGAC 2940  
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Qy 2941 ACATGCCAATGACGAAGTACCAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA 3000  
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Qy 3001 CGGTTTGGTGGAAAGCATATACAGAGCTATCTTATCTATCAAGTGTCAACATCTCTTA 3060  
Db 7498 CGGTTTGGTGGAAAGCATATACAGAGCTATCTTATCTATCAAGTGTCAACATCTCTTA 7557  
Qy 3061 GGGGAGAACCCGATCTGACTGTATCCGCCCAACAGTCACTCATGSGGGCCGAAGGC 3120  
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Qy 3121 AGAATTTCAAGAGGACATCTCATTTCTTGTATCAAGAGGCTCATCTTCTCT 3180  
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Qy 3241 ACATTCATGCTTCACTCGGCGAGTATCCCTTGCAGGCTTGCAGCAAGATGCCCC 3300  
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Db 7798 AACTGTGTATTAAGAGTGTATACAGATTCATATCCCTAATCTTCTATAGAAACC 7855  
RESULT 5  
US-10-824-782-134  
; Sequence 134, Application US/10824782  
; Publication No. US20040234552A1  
; GENERAL INFORMATION:  
; APPLICANT: Peeters, Bernadus; de Leeuw, Olav; Klaus, Guus; Gielkens, Arnold  
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic  
; FILE REFERENCE: 2183-4646US  
; CURRENT APPLICATION NUMBER: US/10/824,782  
; PRIOR FILING DATE: 2004-04-15  
; PRIOR APPLICATION NUMBER: US/10/788,232  
; PRIOR FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: PCT/NL99/00377  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 134  
; LENGTH: 15186  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus strain LaSota  
US-10-824-782-134  
Query Match 99.9%; Score 3353.2; DB 8; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ACGGGTGAAGATTTCTGATATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
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Db 4558 TTCTACCAAGAACCCAGCACTATGATGTGACTATCCGGATTGCGCTGCACTGAGTTG 4617  
Qy 121 CATCTGTCCGCAAACTCCATTGATGAGGAGGCTCTTTGACGTCGAGAAATGTGTTAC 180  
Db 4618 CATCTGTCCGCAAACTCCATTGATGAGGAGGCTCTTTGACGTCGAGAAATGTGTTAC 4677  
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Qy 601 TGTTAATGACCAATTTAATATAACAGTCAAGATTAAGTGTGATCAAAATTTGCACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATATAACAGTCAAGATTAAGTGTGATCAAAATTTGCACAGCA 5157

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QY 961 CTTATCCGTAAAGCAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
DB 5458 CTTATCCGTAAAGCAACAACGAGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 5517  
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DB 5518 GGTCGGTTCGTGTATGAAAGAACTTGACACTCATCTGTATGAAAACTGACTTAGATTT 5577  
QY 1081 ATATTGTATCAAGATATGTAAGTTCCCTATATGCCCTGTGTATTTATTCCTGCTTGAAGGG 1140  
DB 5578 ATATTGTATCAAGATATGTAAGTTCCCTATATGCCCTGTGTATTTATTCCTGCTTGAAGGG 5637  
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DB 5638 CAATAGCTCGGCTGTATGTACTCAAAAGACGAAAGGCGCACTTACTACACCATCATGAC 5697  
QY 1201 TATCAAAAGTTCACTCATCTCGCAACCTGCAGATGACAATGTAGATGTGTAAACCCCCC 1260  
DB 5698 TATCAAAAGTTCACTCATCTCGCAACCTGCAGATGACAATGTAGATGTGTAAACCCCCC 5757  
QY 1261 GGGTATCATATCGCAAAACTATGGAAGACCGGTCTCTTAATAGATTAACAATCATGTGCA 1320  
DB 5758 GGGTATCATATCGCAAAACTATGGAAGACCGGTCTCTTAATAGATTAACAATCATGTGCA 5817  
QY 1321 TGTTTATCTTTAGCGGGAATTAATTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCA 1380  
DB 5818 TGTTTATCTTTAGCGGGAATTAATTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCA 5877  
QY 1381 GAAGAAATATCTCAATACAGATTTCTCAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 1440  
DB 5878 GAAGAAATATCTCAATACAGATTTCTCAAGTAAATTAACAAGGCAATCTTGATATCTCAAC 5937  
QY 1441 TGAAGTTGGGAATGTCAACAATCGATCATGAATGCTTTGAATAGTTAGAGAAAGCAA 1500  
DB 5938 TGAAGTTGGGAATGTCAACAATCGATCATGAATGCTTTGAATAGTTAGAGAAAGCAA 5997  
QY 1501 CAGAAACTAGCAAAAGTCAATGTCAAACTGACTAGCAATCTCTCTCATTTACTTATAT 1560  
DB 5998 CAGAAACTAGCAAAAGTCAATGTCAAACTGACTAGCAATCTCTCTCATTTACTTATAT 6057  
QY 1561 CGTTTGAATCATATCTCTTGTGTTTGTATGATTAAGCTGATTTCTAGATGCTACTACT 1620  
DB 6058 CGTTTGAATCATATCTCTTGTGTTTGTATGATTAAGCTGATTTCTAGATGCTACTACT 6117  
QY 1621 AATGTACAAGCAAAAGGCGCAAAAACCTTATTTATGCTTGGGAATTAATCTAGAGA 1680  
DB 6118 AATGTACAAGCAAAAGGCGCAAAAACCTTATTTATGCTTGGGAATTAATCTAGAGA 6177  
QY 1681 TCAGATGAGGCACTTACAAAATGTGAAACAAGATGAGAAAGAGGTTTCCCTAATAG 1740  
DB 6178 TCAGATGAGGCACTTACAAAATGTGAAACAAGATGAGAAAGAGGTTTCCCTAATAG 6237  
QY 1741 TAATTGTGTGAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACTACCGGT 1800

DB 6238 TAATTGTGTGAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAACTACCGGT 6297  
QY 1801 TGTATGATGACCAAGAGACGATATATCGGGTAAACGGTAAAGAGAGCCGCCCTCAATTGC 1860  
DB 6298 TGTATGATGACCAAGAGAGATATACGGGTAAACGGTAAAGAGAGAGCCGCCCTCAATTGC 6357  
QY 1861 GAGCCAGGCTTCAACACTCCGTTCTACCGGTTACCGGACCAACAGTCTCATATCGGAC 1920  
DB 6358 GAGCCAGGCTTCAACACTCCGTTCTACCGGTTACCGGACCAACAGTCTCATATCGGAC 6417  
QY 1921 CGCGCCGTTAGCCAAAGTTGGGTTAGAAATGATAAGAGAGGGAATAAATACATGGCGC 1980  
DB 6418 CGCGCCGTTAGCCAAAGTTGGGTTAGAAATGATAAGAGAGGGAATAAATACATGGCGC 6477  
QY 1981 TTGATATTTCCGATTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGAGCC 2040  
DB 6478 TTGATATTTCCGATTTGCAATCTTATTTCTTAAACAGTATGACCTTGGCTATATCTGAGCC 6537  
QY 2041 TCCCTTTTATATAGCATAGGGGGCTAGACACACTAGCCATCTTGTAGGCAATCCGACTAGG 2100  
DB 6538 TCCCTTTTATATAGCATAGGGGGCTAGACACACTAGCCATCTTGTAGGCAATCCGACTAGG 6597  
QY 2101 ATTTCCAGGGGAGAAAGAAAGATTAATCATCTACCTTGGTTCCATCAAGATGTAGAT 2160  
DB 6598 ATTTCCAGGGGAGAAAGAAAGATTAATCATCTACCTTGGTTCCATCAAGATGTAGAT 6657  
QY 2161 AGGATATATTAAGCAAGTGGCCCTGAGTCTCGTTGGCATTTGTAATTAATCTAGAGCACA 2220  
DB 6658 AGGATATATTAAGCAAGTGGCCCTGAGTCTCGTTGGCATTTGTAATTAATCTAGAGCACA 6717  
QY 2221 ATTATGAACGCAATTAACATCTCTCTTATAGATTAATGAGGCTGCAAAACAAGTGGG 2280  
DB 6718 ATTATGAACGCAATTAACATCTCTCTTATAGATTAATGAGGCTGCAAAACAAGTGGG 6777  
QY 2281 TGGGGGGCACTTATCTATGACCCAGATTAATAGGGGGGATAGGCAAAAGAACTGATGTA 2340  
DB 6778 TGGGGGGCACTTATCTATGACCCAGATTAATAGGGGGGATAGGCAAAAGAACTGATGTA 6837  
QY 2341 GATGATGCTATGATATGATGATCAATCTATGATCCCTGCTGCAATTTCAAGAAACATCTGAATTT 2400  
DB 6838 GATGATGCTATGATATGATGATCAATCTATGATCCCTGCTGCAATTTCAAGAAACATCTGAATTT 6897  
QY 2401 ATCCCGGCGCTTACTACAGATCAGTTGCACTCGAATATCCCTGATTTGACATGAGTGT 2460  
DB 6898 ATCCCGGCGCTTACTACAGATCAGTTGCACTCGAATATCCCTGATTTGACATGAGTGT 6957  
QY 2461 ACCCATTAATGCTACACCCATATGTAATTTGTCTGATGACAGATCACTCACTATCA 2520  
DB 6958 ACCCATTAATGCTACACCCATATGTAATTTGTCTGATGACAGATCACTCACTATCA 7017  
QY 2521 TATGATTAATTTAGCATTTGGTGTGCTCCGACATCTGCAACAGGAGAGGATTTCTTTTCT 2580  
DB 7018 TATGATTAATTTAGCATTTGGTGTGCTCCGACATCTGCAACAGGAGAGGATTTCTTTTCT 7077  
QY 2581 ACTGCGGTTCCATCAACTGAGACGACACCCAAATGGAAGTCTTGCAAGTGTAGTGA 2640  
DB 7078 ACTGCGGTTCCATCAACTGAGACGACACCCAAATGGAAGTCTTGCAAGTGTAGTGA 7137  
QY 2641 ACTCCCTGGGTTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGATTTAT 2700  
DB 7138 ACTCCCTGGGTTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGAAAGATTTAT 7197  
QY 2701 AACTCAGCTGTCCCTACCGGATGTATCAATGGAGGTTTAGGTTTCAGCGCACTACAC 2760  
DB 7198 AACTCAGCTGTCCCTACCGGATGTATCAATGGAGGTTTAGGTTTCAGCGCACTACAC 7257  
QY 2761 GAAAGAGACTTATGATGATCAACAATTTATGCGGGAAGTGGGAGCACTACCGAGAGTA 2820  
DB 7258 GAAAGAGACTTATGATGATCAACAATTTATGCGGGAAGTGGGAGCACTACCGAGAGTA 7317  
QY 2821 GGGGGTGAATCTTTATTTGACAGCGCGGTATGTTCTCAGTCTACGAGGAGGTTAAACCC 2880

Db 7318 GGGGGTGGATCTTTTATTTGAACGCGGATGTTCTCACTGATCTACGAGGGTTAAAAACC 73177  
Qy 2881 AATTCAACCACTGACACTGTACAGGAAGGAATATGTATATATCAAGCATACATGAC 2940  
Db 7378 AATTCAACCACTGACACTGTACAGGAAGGAATATGTATATATCAAGCATACATGAC 7437  
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTGGAATGCGCAAGTCTTGATTAAGCCTGGA 3000  
Db 7438 ACATGCCAGATGAGCAAGACTACAGATTGGAATGCGCAAGTCTTGATTAAGCCTGGA 7497  
Qy 3001 CGGTTTGGTGGAAAGCCATACAGCAAGCATCTTATCTATCAAGGTGCAACATCTCTTA 3060  
Db 7498 CGGTTTGGTGGAAAGCCATACAGCAAGCATCTTATCTATCAAGGTGCAACATCTCTTA 7557  
Qy 3061 GGGGAAGACCCGGATCTGACTGTACCGCCCAACAGTCACTCATGSGGGGCGGAAGGC 3120  
Db 7558 GGGGAAGACCCGGATCTGACTGTACCGCCCAACAGTCACTCATGSGGGGCGGAAGGC 7617  
Qy 3121 AGAATCTCAAGTAGGAGACATCTCATTTCTGTATCAACGAGGGTCATCACTTCTCT 3180  
Db 7618 AGAATCTCAAGTAGGAGACATCTCATTTCTGTATCAACGAGGGTCATCACTTCTCT 7677  
Qy 3181 CCGCGGTTATTAATCTCTATGACAGTACGAACAACACGCACTCTTCAATAGTCTTAT 3240  
Db 7678 CCGCGGTTATTAATCTCTATGACAGTACGAACAACACGCACTCTTCAATAGTCTTAT 7737  
Qy 3241 ACATTCATGCTTCACTCGGCGCAGTAGTATCCCTTGCCAGGCTTGACGAAGATGCCCC 3300  
Db 7738 ACATTCATGCTTCACTCGGCGCAGTAGTATCCCTTGCCAGGCTTGACGAAGATGCCCC 7797  
Qy 3301 AACTCGTGTACTGTAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358  
Db 7798 AACTCGTGTACTGTAGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 6  
US-10-788-232-134  
/ Sequence 134, Application US/10788232  
/ Publication No. US20040235134A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Peeters, Bernadus; de Leeuw, Olav; Klaus, Gius; Gielkens, Armond  
/ TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnosti  
/ FILE REFERENCE: 2183-4646US  
/ CURRENT APPLICATION NUMBER: US/10/788, 232  
/ CURRENT FILING DATE: 2004-02-26  
/ PRIOR APPLICATION NUMBER: PCT/NL99/00377  
/ PRIOR FILING DATE: 1999-06-17  
/ NUMBER OF SEQ ID NOS: 150  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO: 134  
/ LENGTH: 15186  
/ TYPE: DNA  
/ ORGANISM: Newcastle disease virus strain LaSota  
US-10-788-232-134

Query Match 99.9%; Score 3353.2; DB 8; Length 15186;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACCGGGTAAAGATTCTGGATCCGGTTCGGCCCTCCAGGTGCAAGATGGGCTTCAGACC 60  
Db 4498 ACCGGGTAAAGATTCTGGATCCGGTTCGGCCCTCCAGGTGCAAGATGGGCTTCAGACC 4557  
Qy 61 TTCTACCAAGAACCCAGCACTATGATGCTGACATCCGGGTTCGGCTGCACTGAATTG 120  
Db 4558 TTCTACCAAGAACCCAGCACTATGATGCTGACATCCGGGTTCGGCTGCACTGAATTG 4617  
Qy 121 CATCTGCGGCAAACTCATTTGTCAGAGGCTCTTGACAGTGCAGAAATTTGTGTAC 180  
Db 4618 CATCTGCGGCAAACTCATTTGTCAGAGGCTCTTGACAGTGCAGAAATTTGTGTAC 4677  
Qy 181 AGGAGCAAAAGCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 240  
Db 181 AGGAGCAAAAGCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 240

Db 4678 AGGAGCAAAAGCGTCAACATATACCTCATCCAGACAGATCAATCATAGTTAAGCT 4737  
Qy 241 CCTCCCAATCTGCCCAAGATTAAGAGGATGTGCCAAAGCCCTTGATGATACAA 300  
Db 4738 CCTCCCAATCTGCCCAAGATTAAGAGGATGTGCCAAAGCCCTTGATGATACAA 4797  
Qy 301 CAGGACATTGACCACTTGTCTACCCCCCTTGCTGACTTATCCGTATGATACAGAGTGC 360  
Db 4798 CAGGACATTGACCACTTGTCTACCCCCCTTGCTGACTTATCCGTATGATACAGAGTGC 4857  
Qy 361 TGTGACTACATCTGGAGGGGGGAGACAGGGGGCGCTTATATGGGCGCATTTATGGCGGTGT 420  
Db 4858 TGTGACTACATCTGGAGGGGGGAGACAGGGGGCGCTTATATGGGCGCATTTATGGCGGTGT 4917  
Qy 421 GGCCTTTGGGGTTGCAACTGCCCCCAAAATTAACAGCGCGGCGAGCTTGATACAAAGCAA 480  
Db 4918 GGCCTTTGGGGTTGCAACTGCCCCCAAAATTAACAGCGCGGCGAGCTTGATACAAAGCAA 4977  
Qy 481 ACAAAATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGAACCAATGAGCTGT 540  
Db 4978 ACAAAATGCTGCCAATCTCTCCGACTTAAAGAGAGCATTTGCCGAACCAATGAGCTGT 5037  
Qy 541 GCATGAGGTGACATGACGGAATTAATCGCAACTAGAGTGGCAGTTGGGAAGATGACAGATT 600  
Db 5038 GCATGAGGTGACATGACGGAATTAATCGCAACTAGAGTGGCAGTTGGGAAGATGACAGATT 5097  
Qy 601 TGTTAATGACCAATTTAATTAACAGCTCAGAAATTAAGCTGCATCAAAATTTGCACAGA 660  
Db 5098 TGTTAATGACCAATTTAATTAACAGCTCAGAAATTAAGCTGCATCAAAATTTGCACAGA 5157  
Qy 661 AGTTGGTGAAGCTCAACCTGTATCTTAACCGAATTTGACTACAGTATTCGAGCCAAAT 720  
Db 5158 AGTTGGTGAAGCTCAACCTGTATCTTAACCGAATTTGACTACAGTATTCGAGCCAAAT 5217  
Qy 721 CACTCACCGCTTTTAAACAAGCTGACTATTAAGGCACTTTAACAATCTAGCTGGTGA 780  
Db 5218 CACTCACCGCTTTTAAACAAGCTGACTATTAAGGCACTTTAACAATCTAGCTGGTGA 5277  
Qy 781 TATGATTAATTAATGACTAAGTATGAGGGAACAATCAACTCAGCTCATTAATCGG 840  
Db 5278 TATGATTAATTAATGACTAAGTATGAGGGAACAATCAACTCAGCTCATTAATCGG 5337  
Qy 841 TACCGGCTTAATCAACCGGTAAACCTTAATTTATACGACTCAGACTCACTCTTGCGTAT 900  
Db 5338 TACCGGCTTAATCAACCGGTAAACCTTAATTTATACGACTCAGACTCACTCTTGCGTAT 5397  
Qy 901 ACAGGTAACTCTACCTTCACTGCGGGAACCTTAATTAATGCGGCCACTACTTGGAAAC 960  
Db 5398 ACAGGTAACTCTACCTTCACTGCGGGAACCTTAATTAATGCGGCCACTACTTGGAAAC 5457  
Qy 961 CTATCCGTAAAGCAACAGGGGAATTTGCTCGGCACTTGTCCCAAAAGTGTGACACA 1020  
Db 5458 CTATCCGTAAAGCAACAGGGGAATTTGCTCGGCACTTGTGTCCCAAAAGTGTGACACA 5517  
Qy 1021 GGTGCTTCTGTGATTAAGAACTTGAACCTTGACACTCATCTGATTAAGAACTGACTTAATTT 1080  
Db 5518 GGTGCTTCTGTGATTAAGAACTTGAACCTTGACACTCATCTGATTAAGAACTGACTTAATTT 5577  
Qy 1081 ATATTGTGAAGAAATGTAAAGTTCCTTAATGTCCTCGATTAATTTATCCGCTTGAGCGG 1140  
Db 5578 ATATTGTGAAGAAATGTAAAGTTCCTTAATGTCCTCGATTAATTTATCCGCTTGAGCGG 5637  
Qy 1141 CAATACGTCGGCTGTATGTAATCAAGACCGAAGGCGCACTTATCAACATATGATGAC 1200  
Db 5638 CAATACGTCGGCTGTATGTAATCAAGACCGAAGGCGCACTTATCAACATATGATGAC 5697  
Qy 1201 TATCAAGGTTCACTGATGCACTGCAAGATGACCAATGATGATGTAACCCCCC 1260  
Db 5698 TATCAAGGTTCACTGATGCACTGCAAGATGACCAATGATGATGTAACCCCCC 5757  
Qy 1261 GGGTATCATATCGCAAAACTATGAGAAAGCGGTCTCTTAATGATTAACATCATGCAA 1320  
Db 5758 GGGTATCATATCGCAAAACTATGAGAAAGCGGTCTCTTAATGATTAACATCATGCAA 5817

Qy	1321	TGTTTATTCCTTAAGCGGGATTAACCTTTAAAGGCTGAGTGGGAATTCGATGTAACCTTAACA	1380
Dp	5818	TGTTTTATCCTTAAGCGGGATTAACCTTTAAAGGCTGAGTGGGAATTCGATGTAACCTTAACA	5877
Qy	1381	GAAGATATCTCAATATACAAAGATTCTCAAGTATATATAACAGGCATCTTGATATCTCAAC	1440
Dp	5878	GAAGATATCTCAATATACAAAGATTCTCAAGTATATATAACAGGCATCTTGATATCTCAAC	5937
Qy	1441	TGAGCTTGGGAATGTCAACAACCTGATCAGTATATCTTTGAATTAAGTTAGAGAAAGCA	1500
Dp	5938	TGAGCTTGGGAATGTCAACAACCTGATCAGTATATCTTTGAATTAAGTTAGAGAAAGCA	5997
Qy	1501	CAGAAAACCTACACAAGATCAATGTCAACCTGATACGACATCTGCTCCATTACCTATAT	1566
Dp	5998	CAGAAAACCTACACAAGATCAATGTCAACCTGATACGACATCTGCTCCATTACCTATAT	6057
Qy	1561	CGTTTTGACATACATCTCTTGTTTTTGATATCTTAAGCCTGATTTAGAGATGCTACCT	1620
Dp	6058	CGTTTTGACATACATATCTCTTGTTTTTGATATCTTAAGCCTGATTTAGAGATGCTACCT	6117
Qy	1621	AATGTACAGCAAAAGCGCAACAACCTTATATAGCTTGGGAATTAATCTTACA	1680
Dp	6118	AATGTACAGCAAAAGCGCAACAACCTTATATATAGCTTGGGAATTAATATCTTACA	6177
Qy	1681	TCAGATGAGCCCTACACAAAATGTGAACACAGATGAGAACAGAGTTTCCCTAATAG	1740
Dp	6178	TCAGATGAGCCCTACACAAAATGTGAACACAGATGAGAACAGAGTTTCCCTAATAG	6237
Qy	1741	TAAATTTGATGAAGTTCTGGTAGTCTGTCAAGTCAAGAGATTGAAGAAAACCTACCGGT	1800
Dp	6238	TAAATTTGATGAAGTTCTGGTAGTCTGTCAAGTCAAGAGATTGAAGAAAACCTACCGGT	6297
Qy	1801	TGTAGATGACCAAAAGACGATATAACGGGTAGAACCGTAAAGAGAGCGCCCTCAATTGC	1860
Dp	6298	TGTAGATGACCAAAAGACGATATATACGGGTAGAACCGTAAAGAGAGCGCCCTCAATTGC	6357
Qy	1861	GAGCCAGGCTTCAACAACCTCCGTTTCAACCGCTTCAACCGACACACAGTCTCAATCATGGAAC	1922
Dp	6358	GAGCCAGGCTTCAACAACCTCCGTTTCAACCGCTTCAACCGACACACAGTCTCAATCATGGAAC	6417
Qy	1921	CGCCGCCGTTACCAAGTTGCGTTAGAGATGATGAAAGAGGGCAAAAATCATAGGGGC	1980
Dp	6418	CGCCGCCGTTACCAAGTTGCGTTAGAGATGATGAAAGAGGGCAAAAATCATAGGGGC	6477
Qy	1981	TTGATATATCCGGAATTGCAATCTTATTTCTTAAACAGTAGAGACCTTGGCTATATCTGTAGCC	2040
Dp	6478	TTGATATATCCGGAATTGCAATCTTATTTCTTAAACAGTAGAGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTATATAGCATGAGGCGCTTAGACAACCTAGCGATCTTGTAGGCATACCGACTAGG	2100
Dp	6538	TCCCTTTATATAGCATGAGGCGCTTAGACAACCTAGCGATCTTGTAGGCATACCGACTAGG	6597
Qy	2101	ATTTCCAGGGCAAGAAAGATTACATCTACACTTGGTTCCATACAGATGTAGTACAT	2166
Dp	6598	ATTTCCAGGGCAAGAAAGATTACATCTACACTTGGTTCCATACAGATGTAGTACAT	6657
Qy	2161	AGGATATATTAAGCAAGTGCGCCCTTGAGTCTCCGTTGGGATGTTTAAATATCGAGACACA	2222
Dp	6658	AGGATATATTAAGCAAGTGCGCCCTTGAGTCTCCGTTGGGATGTTTAAATATCGAGACACA	6717
Qy	2221	ATTATGAACGCAATTAACATCTCTCTCTTATCAGATTAAATGAGACTGCAACACACAGTGGG	2288
Dp	6718	ATTATGAACGCAATTAACATCTCTCTCTTATCAGATTAAATGAGAGCTGCAACACACAGTGGG	6777
Qy	2281	TGGGGGGCACTTATCATAGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2346
Dp	6778	TGGGGGGCACTTATCATAGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837
Qy	2341	GATGATGCTAGTAGTGCATCATCTTATCCTCTGCAATTTCAAGAACATCTGAATTTT	2400
Dp	6838	GATGATGCTAGTAGTGCATCATCTTATCCTCTGCAATTTCAAGAACATCTGAATTTT	6897

QY	2401	ATCCCGCGCCTAATCAAGATCAAGTTGCACTGGAAATACCTCATTTTGAATGATGTC	2460
Db	6898	ATCCCGCGCCTAATCAAGATCAAGTTGCACTGGAAATACCTCATTTTGAATGATGTC	6955
QY	2461	ACCATTACTGCTACACCCATATATGTCTCGATGACAGATCACTCACTTCA	2520
Db	6958	ACCATTACTGCTACACCCATATATGTCTCGATGACAGATCACTCACTTCA	7017
QY	2521	TATCAGTATTTAGACTTGTGTGTCCTCCGACATCTGCACAGAGAGGTATTTCTTCT	2580
Db	7018	TATCAGTATTTAGACTTGTGTGTCCTCCGACATCTGCACAGAGAGGTATTTCTTCT	7077
QY	2581	ACTCTGGGTTCCATCAACCTGAGACACCACCAATGSAAGTCTTCAGTGTAGTCA	2640
Db	7078	ACTCTGGGTTCCATCAACCTGAGACACCACCAATGSAAGTCTTCAGTGTAGTCA	7137
QY	2641	ACTCCCTCTGGTTGTGATATGCTGTCTCGAAGTCACGAGACAGAGAAAGATTAT	2700
Db	7138	ACTCCCTCTGGTTGTGATATGCTGTCTCGAAGTCACGAGACAGAGAAAGATTAT	7197
QY	2701	AATCTAGTGTCTCTTAGCGCGATGTGTACATGTGGAGTTAAGGTTCGACGGCCATTAAC	2766
Db	7198	AATCTAGTGTCTCTTAGCGCGATGTGTACATGTGGAGTTAAGGTTCGACGGCCATTAAC	7257
QY	2761	GAAAGAGCCATGATGTCACAACTTTTCGGGGACTGGGTGGCCAACTACCCAGAGTA	2820
Db	7258	GAAAGAGCCATGATGTCACAACTTTTCGGGGACTGGGTGGCCAACTACCCAGAGTA	7317
QY	2821	GGGGGTGGATCTTTTATTTGACAGCCCGGTATGTCTTCACTACGAGGGTTAAACC	2880
Db	7318	GGGGGTGGATCTTTTATTTGACAGCCCGGTATGTCTTCACTACGAGGGTTAAACC	7377
QY	2881	AATTCACCCACTGACACTGTACAGGAAGGAAATATGTGATATTAAGCGATTACAATGAC	2940
Db	7378	AATTCACCCACTGACACTGTACAGGAAGGAAATATGTGATATTAAGCGATTACAATGAC	7437
QY	2941	ACATGCCCAATGAGCAAGACTACAGATTGCAATGGCCAAAGTCTTGATTAAGCTTGA	3000
Db	7438	ACATGCCCAATGAGCAAGACTACAGATTGCAATGGCCAAAGTCTTGATTAAGCTTGA	7497
QY	3001	CGTTTGGTGGGAACGCATACAGACAGCTATCTTATCTATCAAGGTGTCAACTCTTAA	3060
Db	7498	CGTTTGGTGGGAACGCATACAGACAGCTATCTTATCTATCAAGGTGTCAACTCTTAA	7557
QY	3061	GGCGAAGACCCGGTACTGACTGTACCGGCCCAACACAGTCACTCATGTGGGGCCGAAGGC	3120
Db	7558	GGCGAAGACCCGGTACTGACTGTACCGGCCCAACACAGTCACTCATGTGGGGCCGAAGGC	7617
QY	3121	AGAAATTCACAGTAGGAGCACTCATTTCTTGATCAAGAGGTCATCACTTCTCT	3180
Db	7618	AGAAATTCACAGTAGGAGCACTCATTTCTTGATCAAGAGGTCATCACTTCTCT	7677
QY	3181	CCCGCGTTATATATATCCATGACAGTCAAGCAAAAAGCCACTCTTCATATGTCCTTAT	3240
Db	7678	CCCGCGTTATATATATCCATGACAGTCAAGCAAAAAGCCACTCTTCATATGTCCTTAT	7737
QY	3241	ACATTCAATGCTTCACTCGGCCAGGTATATCCCTTGCCAGGCTTACGCAAGTCCCC	3300
Db	7738	ACATTCAATGCTTCACTCGGCCAGGTATATCCCTTGCCAGGCTTACGCAAGTCCCC	7797
QY	3301	AACCTGTGTATCTAGAGTCTTAAACAGATCCATATCCCTTAATCTTATATAGAACC	3358
Db	7798	AACCTGTGTATCTAGAGTCTTAAACAGATCCATATCCCTTAATCTTATATAGAACC	7855

RESULT 7  
US-10-440-419-55  
; Sequence 55, Application US/10440419  
; Publication No. US20030224017A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAT, SIBA K.  
; APPLICANT: HUANG, ZHURU  
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS

;; TITLE OF INVENTION: VACCINES OR VACCINE VECTORS  
;; FILE REFERENCE: 108172-00096  
;; CURRENT APPLICATION NUMBER: US/10/440,419  
;; CURRENT FILING DATE: 2003-05-19  
;; PRIOR APPLICATION NUMBER: 09/926,431  
;; PRIOR FILING DATE: 2002-03-06  
;; PRIOR APPLICATION NUMBER: PCT/US00/06700  
;; PRIOR FILING DATE: 2000-05-05  
;; PRIOR APPLICATION NUMBER: 60/381,462  
;; PRIOR FILING DATE: 2002-05-17  
;; PRIOR APPLICATION NUMBER: 60/171,072  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: 60/132,597  
;; PRIOR FILING DATE: 1999-05-05  
;; NUMBER OF SEQ ID NOS: 56  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 55  
;; LENGTH: 15900  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV  
US-10-440-419-55

Query Match 99.7%; Score 3346.8; DB 6; Length 15900;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3351; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ACCGGTGAAGATTCTGGATCCGGCTTGGGCGCTCCAGGTGCAAGATGGGCTCCAGACC 60  
DB 5212 ACCGGTGAAGATTCTGGATCCGGCTTGGGCGCTCCAGGTGCAAGATGGGCTCCAGACC 5271  
QY 61 TTCTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTTGCGCTGGCATGAGTTG 120  
DB 5272 TTCTACCAAGAACCCAGACCTATGATGCTGATCTATCCGGGTTGCGCTGGCATGAGTTG 5331  
QY 121 CATCTGTCGGGCAAACTCTCATTTGATGCGAGGCTCTTGGCACTGCAAGAAATTGGTTAC 180  
DB 5332 CATCTGTCGGGCAAACTCTCATTTGATGCGAGGCTCTTGGCACTGCAAGAAATTGGTTAC 5391  
QY 181 AGGAGCAAAAGCGGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240  
DB 5392 AGGAGCAAAAGCGGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 5451  
QY 241 CCTCCGCAATCTGCCCAAGATTAAGAGCATGTGCGAAAGCCCTTGGATGATACAA 300  
DB 5452 CTTCCGCAATCTGCCCAAGATTAAGAGCATGTGCGAAAGCCCTTGGATGATACAA 5511  
QY 301 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGATACAAAGTGC 360  
DB 5512 CAGGACATTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGTAGATACAAAGTGC 5571  
QY 361 TGTGACATCACTGGAGGGGGAGACAGGGGCGCTTATAGGGGCTTATTTGGCGGTGT 420  
DB 5572 TGTGACATCACTGGAGGGGGAGACAGGGGCGCTTATAGGGGCTTATTTGGCGGTGT 5631  
QY 421 GGCTCTTGGGGTTGCACTGCCGCAAAATTAACAGCGCGCGCACTCTGATACAAAGCAA 480  
DB 5632 GGCTCTTGGGGTTGCACTGCCGCAAAATTAACAGCGCGCGCACTCTGATACAAAGCAA 5691  
QY 481 ACAAAATGCTGCCAATCTCTCCGACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 540  
DB 5692 ACAAAATGCTGCCAATCTCTCCGACTTTAAAGAGAGCATTTGCCGAACCAATGAGGCTGT 5751  
QY 541 GCATGAGGTGACGAGGATTAATGCGCACTAGCAGTGGCGAGTTGGGAAGATGACGAGTT 600  
DB 5752 GCATGAGGTGACGAGGATTAATGCGCACTAGCAGTGGCGAGTTGGGAAGATGACGAGTT 5811  
QY 601 TGTAAATGACCAATTTATATAAAACAGCTCAGAAATTAAGATGATCAAAATTTGACAGCA 660  
DB 5812 TGTAAATGACCAATTTATATAAAACAGCTCAGAAATTAAGATGATCAAAATTTGACAGCA 5871  
QY 661 AGTTGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGAGCACAAAAT 720

DB 5872 AGTTGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGAGCACAAAAT 5931  
QY 721 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAAATCTAGCTGTGGAAA 780  
DB 5932 CACTTCACTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAAATCTAGCTGTGGAAA 5991  
QY 781 TATGATTAATCTTATTTGACTAAGTATGATGAGGAAACAATCAACTCAGCTCATTAATCGG 840  
DB 5992 TATGATTAATCTTATTTGACTAAGTATGATGAGGAAACAATCAACTCAGCTCATTAATCGG 6051  
QY 841 TAGCGCTTATCAACCGGTAACTTATCTATACACTCAGACTCACTGAGTAT 900  
DB 6052 TAGCGCTTATCAACCGGTAACTTATCTATACACTCAGACTCACTGAGTAT 6111  
QY 901 ACAAGTAATCTACCTTCAGTGGGAACTTAATATATATGCTGCCACTTATGGAAC 960  
DB 6112 ACAAGTAATCTACCTTCAGTGGGAACTTAATATATATGCTGCCACTTATGGAAC 6171  
QY 961 CTTATCCGTAAAGCAACCAAGGGATTTGCTGGGCACTTGTCCCAAAAGTGGACACA 1020  
DB 6172 CTTATCCGTAAAGCAACCAAGGGATTTGCTGGGCACTTGTCCCAAAAGTGGACACA 6231  
QY 1021 GGTGGTTCTGTGATGAGAAGACTTGACACCTCATCTGATATAGAACTGACTAGATT 1080  
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DB 6292 ATATTGTACAAGATATAGTAAGTTCCTATATGCTCCCTGTATTTATCTGCTTGAACGG 6351  
QY 1141 CAATACGTCGCTGTATGTATCTAAAGACCGAAGGGCACTTATACCATATCATGAC 1200  
DB 6352 CAATACGTCGCTGTATGTATCTAAAGACCGAAGGGCACTTATACCATATCATGAC 6411  
QY 1201 TATCAAAAGTTCACTGATGCGCAACTGCAAGATGACAAACATGTGATGTGTAACCCGCC 1260  
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QY 1261 GGGTATCATATCGCAAAACTATGAGAGAGCGGTCTCTATATAGATTAACAATCATGACAA 1320  
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QY 1321 TGTATTATCTTATAGCGGGAATTAATTAAAGCTCAGTGGGGAATTCATGTAATTTC 1380  
DB 6532 TGTATTATCTTATAGCGGGAATTAATTAAAGCTCAGTGGGGAATTCATGTAATTTC 6591  
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DB 6592 GAGGAATATCTCAATTAAGAATCTCAAGTAATTAACAAGGCAATCTGTATCTCAAC 6651  
QY 1441 TGAGCTTGGGATGTCAACAACCTCGATCAGTAATGCTTTGAATAGTTAGAGAAACAA 1500  
DB 6652 TGAGCTTGGGATGTCAACAACCTCGATCAGTAATGCTTTGAATAGTTAGAGAAACAA 6711  
QY 1501 CAGAAAACTAGCAAACTCAATGTAAGTCAACTGACTAGCAATCTGCTCTCATTAATCT 1560  
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QY 1561 CGTTTGAATCAATATCTCTGTTTGGTATTAATAGCTGATTTAGAGTCTGACT 1620  
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DB 6832 AATGTACAAAGCAAAAGCGCAACAAAGCTTATTAATGCTTGGGAATTAATCTTGA 6891  
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DB 6892 TCAGATGAGGCACTTACAAAAATGTGAAACAGATGAGGAGCAAGGTTTCCCTAATAG 6951  
QY 1741 TAATTTGTGGAAGTTCTGTAGTCTGTCAAGTTCAAGAGTTTAAGAAAACTAACCGGT 1800



Db 6952 TAATTTGTGAAAGTTCTGTAGTCTGTCACTTCAGAGATTAAAGAAAACTACCGCT 7011  
Qy 1801 TGTAGATGACCAAGAGAGATATACGGGTAGACGGTAAGAGAGCCGCCCTCAATTGC 1860  
Db 7012 TGTAGATGACCAAGAGAGATATACGGGTAGACGGTAAGAGAGCCGCCCTCAATTGC 7071  
Qy 1861 GAGCAGAGCTTACACACTCCGTTCTACCGCTTACCGGACCAAGTCTCATATGAGAC 1920  
Db 7072 GAGCAGAGCTTACACACTCCGTTCTACCGCTTACCGGACCAAGTCTCATATGAGAC 7131  
Qy 1921 CGGCGCGGTAGCCAGATTGCGTTAGAGATGATGAAGAGAGGAAAAAATACATGGCGC 1980  
Db 7132 CGGCGCGGTAGCCAGATTGCGTTAGAGATGATGAAGAGAGGAAAAAATACATGGCGC 7191  
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Db 7192 TTGATATTCGGGATTGCAATCTTATTTCTTAAACAGTAGACCTTGGCTATATCTGAGCC 7251  
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGACACACTAGCCATCTTGTAGGCAATCCGATAGG 2100  
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Qy 2101 ATTTCAGGGAGAGAAAGAAATTAACATCTACCTTGCTTCCATCAAGATGTAGTAT 2160  
Db 7312 ATTTCAGGGAGAGAAAGAAATTAACATCTACCTTGCTTCCATCAAGATGTAGTAT 7371  
Qy 2161 AGGATATATAGCAAGTAGTGGCCCTTGAAGTCTCGTTGGCAATTGTTAAATCTGAGACCA 2220  
Db 7372 AGGATATATAGCAAGTAGTGGCCCTTGAAGTCTCGTTGGCAATTGTTAAATCTGAGACCA 7431  
Qy 2221 ATTATGAACGCATATACATCTCTCTTATCAGATTATAGAGGTGCAACACAGTGGG 2280  
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Qy 2281 TGGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGA 2340  
Db 7492 TGGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGA 7551  
Qy 2341 GATGATGCTATGATGTCATCATCTTCTGATTCCTGTGATTTCAAGAACATCTGAATTTT 2400  
Db 7552 GATGATGCTATGATGTCATCATCTTCTGATTCCTGTGATTTCAAGAACATCTGAATTTT 7611  
Qy 2401 ATCCGGGCGCTACTACAGATCAGGTGCACTGAAATACCTCATTTGACATGATGCT 2460  
Db 7612 ATCCGGGCGCTACTACAGATCAGGTGCACTGAAATACCTCATTTGACATGATGCT 7671  
Qy 2461 ACCCATTAAGTCTACACCCCATATATGTAATATGTTGATGAGATCACTCATATTCA 2520  
Db 7672 ACCCATTAAGTCTACACCCCATATATGTAATATGTTGATGAGATCACTCATATTCA 7731  
Qy 2521 TATCAGATTATAGCATTTGGTGTCTCGGACATCTGCAACAGGGAAGGATTTCTTTTCT 2580  
Db 7732 TATCAGATTATAGCATTTGGTGTCTCGGACATCTGCAACAGGGAAGGATTTCTTTTCT 7791  
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Db 7792 ACTCTGCTTCAATCAACTGAGACAGACCCAAATGCGAAGTCTTGTGACGTGAGTGA 7851  
Qy 2641 ACTCTCTGGGTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTTAT 2700  
Db 7852 ACTCTCTGGGTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGAAAGATTTAT 7911  
Qy 2701 AACTCAGACTGCTTACGCGGATGTACATGAGGAGTTAGGGTTTCAGCGCAATATCAC 2760  
Db 7912 AACTCAGACTGCTTACGCGGATGTACATGAGGAGTTAGGGTTTCAGCGCAATATCAC 7971  
Qy 2761 GAAAGAGACCTAGATGTCACAACTTATTCGGGAGCTGGGTGCGCAACTACCCAGAGTA 2820  
Db 7972 GAAAGAGACCTAGATGTCACAACTTATTCGGGAGCTGGGTGCGCAACTACCCAGAGTA 8031  
Qy 2821 GGGGGGTGATCTTTTATATGACGCGCGATATGTTCTCAGTCTACGAGGGTTAAACC 2880  
Db 8032 GGGGGGTGATCTTTTATATGACGCGCGATATGTTCTCAGTCTACGAGGGTTAAACC 8091

Qy 2881 AATTACCCAGTGAACCTGTACAGAGAAAGGAAATATGTGATATACAGCGATACATGAC 2940  
Db 8092 AATTACCCAGTGAACCTGTACAGAGAAAGGAAATATGTGATATACAGCGATACATGAC 8151  
Qy 2941 ACATGCCAGATGAGCAAGATATACAGATTTGGAATGCGCAAGTCTTGATTAAGCTTGA 3000  
Db 8152 ACATGCCAGATGAGCAAGATATACAGATTTGGAATGCGCAAGTCTTGATTAAGCTTGA 8211  
Qy 3001 CGGTTGTGGGAAAGCATACAGAGCTATCTTATCTATCAAGTGTCAACATCTCTTA 3060  
Db 8212 CGGTTGTGGGAAAGCATACAGAGCTATCTTATCTATCAAGTGTCAACATCTCTTA 8271  
Qy 3061 GGGGAGACCCGTAAGTACTGTACCTGACCGCCCAACACAGTCACTCATAGGGGCGAGAGC 3120  
Db 8272 GGGGAGACCCGTAAGTACTGTACCTGACCGCCCAACACAGTCACTCATAGGGGCGAGAGC 8331  
Qy 3121 AGAATTTCAAGATAGGAGACATCTCATTTCTTGTATGATCAAGAGGGTATCATCTTCT 3180  
Db 8332 AGAATTTCAAGATAGGAGACATCTCATTTCTTGTATCAACAGAGGTATCATCTTCT 8391  
Qy 3181 CCGCGTTATATATATCTTATGACAGTCAAGCAAAACAGGCACTTTCATATGCTTAT 3240  
Db 8392 CCGCGTTATATATATCTTATGACAGTCAAGCAAAACAGGCACTTTCATATGCTTAT 8451  
Qy 3241 ACATTCATGCTTCACTCGCCAGTATATCCCTTGCAGGCTTACAGCAAGATGCCCC 3300  
Db 8452 ACATTCATGCTTCACTCGCCAGTATATCCCTTGCAGGCTTACAGCAAGATGCCCC 8511  
Qy 3301 AACTGTTGTATCTGAGATCTATACAGATTCATATCCCTATATCTTATAGAAAC 3358  
Db 8512 AACTGTTGTATCTGAGATCTATACAGATTCATATCCCTATATCTTATAGAAAC 8569

RESULT 8  
US-10-440-419-56  
; Sequence 56, Application US/10440419  
; Publication No. US20030224017A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, SIBA K.  
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USERFUL AS  
; FILE REFERENCE: 108172-00096  
; CURRENT APPLICATION NUMBER: US/10/440, 419  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 09/926, 431  
; PRIOR FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: PCT/US00/06700  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/381, 462  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/171, 072  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: 60/132, 597  
; PRIOR FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 15882  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV  
US-10-440-419-56  
Query Match 95.2%; Score 3198; DB 6; Length 15882;  
Best Local Similarity 97.0%; Pred. No. 0;  
Matches 3256; Conservative 0; Mismatches 100; Indels 0; Gaps 0;  
Qy 1 ACGGGTAGAAGATTCTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60  
Db 4498 ACGGGTAGAAGATTCTGATCCCGGTTGGCGCCCTTCTTAGGTGCAAGATGGGCCCCAGACC 4557



QY 61 TTCTACCAAGAACCCAGACCTTATGATGCTGATCTATCCGGGTGCGCTGSCACTGAGTTG 120  
Db 4558 TTCTACCAAGAACCCAGATACCTATGATGCTGATCTGCTCGAGTCCGCTGGTACTGAGTTG 4617  
QY 121 CATCTGTCGGGCAAACTCCATTTGATGCGAGGCTCTTGCGACTGACGAAATTTGGTTAC 180  
Db 4618 CATCTGTCGGGCAAACTCCATTTGATGCGAGGCTCTTGCGACTGACGAAATTTGGTTAC 4677  
QY 181 AGGAGACAAAGCCGTCACATATATACCTCATCCGACAGGATCAATCATATGTTAAGCT 240  
Db 4678 AGGAGACAAAGCCGTCACATATATACCTCATCCGACAGGATCAATCATATGTTAAGCT 4737  
QY 241 CTTCCCGAATCTGCGCAAGGATGAAGGCAATGCGAAGAGCCCTTGATGATCAAA 300  
Db 4738 CTTCCCGAATCTGCGCAAGGATGAAGGCAATGCGAAGAGCCCTTGATGATCAAA 4797  
QY 301 CAGGACATTGACCACTTTTGCTCAACCCCTTGTTGATCTCTATCCGTAGATACAAAGATC 360  
Db 4798 CAGGACATTGACCACTTTTGCTCAACCCCTTGTTGATCTCTATCCGTAGATACAAAGATC 4857  
QY 361 TGTGACTACATCTTGAGGGGGAGACAGGGGCGCTTATAGAGCGCCATTTATTTGGCGGTG 420  
Db 4858 TGTGACTACATCTTGAGGGGGAGACAGGGGCGCTTATAGAGCGCCATTTATTTGGCGGTG 4917  
QY 421 GGCCTTTGGGGTTGCAACTGCGGCAAAATTAACGCGCGCAGCTCTGATACAAAGCAA 480  
Db 4918 GGCCTTTGGGGTTGCAACTGCGGCAAAATTAACGCGCGCAGCTCTGATACAAAGCAA 4977  
QY 481 ACAAAATGCTGCCCAACATCTCTCCGACTTTAAAGAGACATTCGCCCAACCAATGAGGCTGT 540  
Db 4978 ACAAAATGCTGCCCAACATCTCTCCGACTTTAAAGAGACATTCGCCCAACCAATGAGGCGGT 5037  
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QY 601 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAAGACTGATCAAAATTTGCACAGCA 660  
Db 5098 TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAAGACTGATCAAAATTTGCACAGCA 5157  
QY 661 AGTTGGTGTAGAGTCAACCTGTACTTAACGGAATTTGACTACAGTATTTGGACCAAAAT 720  
Db 5158 AGTTGGTGTAGAGTCAACCTGTACTTAACGGAATTTGACTACAGTATTTGGACCAAAAT 5217  
QY 721 CACTTCACTGCTTTAAACAGGTGACTATTCAGGCACTTTTACATCTAGCTGTGGAAA 780  
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QY 1321 TGTTTTATCTTATGAGCGGGATTAATTTAAGCTCTAGGGGGAATTCGATGTAACTTATCA 1380  
Db 5818 TGTTTTATCTTATGAGCGGGATTAATTTAAGCTCTAGGGGGAATTCGATGTAACTTATCA 5877  
QY 1381 GAAGAAATATCTCAATACAGATTTCTCAAGTATTAATAAGGCAATCTGATATCTCAAC 1440  
Db 5878 GAAGAAATATCTCAATACAGATTTCTCAAGTATTAATAAGGCAATCTGATATCTCAAC 5937  
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Db 6298 TGTAGATGACAAAGACGATATACGGGTAGAAACGGTAAAGAGGCCGCCCTCAATTCG 6357  
QY 1861 GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCAATATGAGAC 1920  
Db 6358 GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTCAACGACCAACAGTCTCAATATGAGAC 6417  
QY 1921 CGGCGGTTAGGCAAGTTGCTTGAAGATGATGAAGAGGCAAAATTAACATGCGCG 1980  
Db 6418 CGGCGGTTAGGCAAGTTGCTTGAAGATGATGAAGAGGCAAAATTAACATGCGCG 6477  
QY 1981 TTGATATTCGGAATTTGCAATCTTATTAACAGTATGACTTGGCTATATCTGTAGCC 2040  
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QY 2041 TCCCTTTATATAGCATGCGGGCTAGACACACTAGCGATTTGTAGGCAATCCGACTAGG 2100  
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QY 2101 AATTTCCAGGCAAGAAAGATTAACATCTACCTGCTTCAATCAAGATGATAGAT 2160  
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QY 2161 AGGATATATTAAGCAAGTGGCCTTGAATCTCCGTTGGCAATTTGTTAAATCTGAGACACA 2220  
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QY 2221 AATATGAACGCAATTAACATCTCTCTTATCAAGATTAATGAGCTGCAAAACAGTGGG 2280

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Qy 2281 TGGGGGGGCACTTATCCATGACCCAGATTAATATAGGGGGGATAGGCAAGAACTCATGTGA 2340  
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Qy 2401 ATCCCGGGGCTTACTACAGATCAGGTTCAGTCTGCAATACCTCATTTGACATGATGCT 2460  
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Qy 2761 GAAAGAGACTAGATGTCACAACTTATTCGGGAGCTGGGAGGAGGAGGAGGAGGAGGAG 2820  
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Qy 3001 CGGTTTGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGGTCTCAACATCTTTTG 3060  
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Qy 3121 AGAATTTCTACAGTAGGAGCACTCTCATTTCTTTGATCAACGAGGCTCATCATCTTCTCT 3180  
Db 7618 AGAATTTCTACAGTAGGAGCACTCTCATTTCTTTGATCAACGAGGCTCATCATCTTCTCT 7677  
Qy 3181 CCCGGTATTAATATCTTATGACAGTCAAGCAAGAAAGCCACTTCTATATGCTCTTAT 3240  
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Db 7738 ACATTCATGCTTACTCGGCAAGTATGATCCCTGCAAGGCTTCAAGCAAGATGCTCC 7797  
Qy 3301 AACTCGTGTGTTACTGAGTCTTATCAGATCCATATCCCTATATCTTCTATTAAGAAC 3358

Db 7798 AACTCGTGTGTTACTGAGTCTTATACAGATCCATATCCCTATCTTCTATTAAGAAC 7855  
RESULT 9  
US-09-881-457A-1  
; Sequence 1, Application US/09881457A  
; Patent No. US20020081316A1  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Cook, Stephanie M  
; APPLICANT: Wild, Marsha A  
; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof  
; FILE REFERENCE: ST0105K10KX  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US/09/881,457A  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/426,352  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/804,372  
; PRIOR FILING DATE: 1997-02-21  
; PRIOR APPLICATION NUMBER: PCT/US95/10245  
; PRIOR FILING DATE: 1995-08-09  
; PRIOR APPLICATION NUMBER: 08/663,566  
; PRIOR FILING DATE: 1996-06-13  
; PRIOR APPLICATION NUMBER: 08/288,065  
; PRIOR FILING DATE: 1994-08-09  
; PRIOR APPLICATION NUMBER: PCT/US93/05681  
; PRIOR FILING DATE: 1993-06-14  
; PRIOR APPLICATION NUMBER: 08/023,610  
; PRIOR FILING DATE: 1993-02-26  
; PRIOR APPLICATION NUMBER: 07/898,087  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3570  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1194)..(2888)  
; OTHER INFORMATION: NDV Fusion Protein  
; NAME/KEY: misc\_feature  
; LOCATION: (1355)  
; OTHER INFORMATION: n = any nucleotide  
US-09-881-457A-1  
Query Match 50.7%; Score 1701.6; DB 3; Length 3570;  
Beet Local Similarity 98.4%; Fred. No. 0;  
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;  
Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGTGGGCTCCAGAACCTTCTACCAAGAACCC 75  
Db 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGTGGGCTCCAGAACCTTCTACCAAGAACCC 1258  
Qy 76 AGACCTATGATGCTGATATCCGGGTTGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 135  
Db 1259 AGACCTATGATGCTGATATCCGGGTTGCGCTGGCACTGAGTTGATCTGTCCGGCAAA 1318  
Qy 136 CTCATTTATGAGCAGGCTCTTTGCAAGCTGCAAGAAATTTGTGTTAAGAGAGCAAGCCGT 195  
Db 1319 CTCATTTATGAGCAGGCTCTTTGCAAGCTGCAAGAAATTTGTGTTAAGAGAGCAAGCCGT 1377  
Qy 196 CAACATATACCTCATCCAGAGACAGATCATCATAGTTAAGTCTCCGAAATCTGCC 255  
Db 1378 CAACATATACCTCATCCAGAGAGG-TCAATCATTA-TTAAAGTCTCTCCGAAATCTGCC 1435  
Qy 256 CAAGATTAAGAGGAGGATGCGAAAGCCCTTGGATGATCAACAGAGACATTGAACA 315  
Db 1436 AAAGATTAAGAGGAGGATGCGAAAGCCCTTGGATGATCAACAGAGACATTGAACA 1495  
Qy 316 TTTGCTCAACCCCTCTTGTGATCTTATCCGTTAGATTAAGAGTGTGAGCTTCAATCTGG 375  
Db 1496 TTTGCTCAACCCCTCTTGTGATCTTATCCGTTAGATTAAGAGTGTGAGCTTCAATCTGG 1555

QY 376 AGGGGGGAGACAGGGGGCGCTTATAGCGCCATTATGGCGGTGTGCTTTGGGGTTGC 435  
DB 1556 AGGGGGGAGACAGGGGGCGCTTATAGGGGCCATTATGGCGGTGTGCTTTGGGGTTGC 1615  
QY 436 AACTGCCGCACTTAATTAACAGGGGGCGGAGCTGTATCAAGCCAAACAAATATGCTGCCAA 495  
DB 1616 AACTGCCGCACTTAATTAACAGGGGGCGGAGCTGTATCAAGCCAAACAAATATGCTGCCAA 1675  
QY 496 CATCTCCGACTTAAGAGACATTTGCCGCAACCAATGAGCTGTGATGAGTCACTGA 555  
DB 1676 CATCTCCGACTTAAGAGAGCAATTTGCCGCAACCAATGAGCTGTGATGAGTCACTGA 1735  
QY 556 CGGATTTTCGCACTAGACAGTGGGAGTTGGGAAAGATGACAGAGTTTGTAAATGCAAT 615  
DB 1736 CGGATTTTCGCACTAGACAGTGGGAGTTGGGAAAGATGACAGAGTTTGTAAATGCAAT 1795  
QY 616 TAATTAACAGCTAGAGAAATTAAGCTGCATCAAAATTTGCAAGAAAGTGTGTAGAGCT 675  
DB 1796 TAATTAACAGCTAGAGAAATTAAGCTGCATCAAAATTTGCAAGAAAGTGTGTAGAGCT 1855  
QY 676 CAACCTGTACTTAACCGAATTTGATACAGTATTCGAGCAACAATCACTTCACTGCTTT 735  
DB 1856 CAACCTGTACTTAACCGAATTTGATACAGTATTCGAGCAACAATCACTTCACTGCTTT 1915  
QY 736 AAACAAGCTGACTATTCAGGCACTTTTCAATCTAGCTGTGGAAATATGATTAATT 795  
DB 1916 AAACAAGCTGACTATTCAGGCACTTTTCAATCTAGCTGTGGAAATATGATTAATT 1975  
QY 796 GACTTAATTTAGTGTAGGAAACATCAACTGACTCATTAATCGGTAGCGGCTTAATCAC 855  
DB 1976 GACTTAATTTAGTGTAGGAAACATCAACTGACTCATTAATCGGTAGCGGCTTAATCAC 2035  
QY 856 CGGTAAACCTATTTATATACAGACTCAAGACTCACTTGGGTATACAGTAACTTACC 915  
DB 2036 CGGTAAACCTATTTATATACAGACTCAAGACTCACTTGGGTATACAGTAACTTACC 2095  
QY 916 TTCACTGGGAACTTAATATATATGCGTCCACTTCTTGAAACCTTATCCGTAAACAC 975  
DB 2096 TTCACTGGGAACTTAATATATATGCGTCCACTTCTTGAAACCTTATCCGTAAACAC 2155  
QY 976 AACCAGGGGATTTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTGGTCTGTGAT 1035  
DB 2156 AACCAGGGGATTTGCTCGGCACTTGTGTCCCAAAAGTGTGACACAGGTGGTCTGTGAT 2215  
QY 1036 AGAAGAACTTGACACTCATATGTATAGAAATGACTTATGATTTATATTTAGCAAGAT 1095  
DB 2216 AGAAGAACTTGACACTCATATGTATAGAAATGACTTATGATTTATATTTAGCAAGAT 2275  
QY 1096 AGTAAAGTTCCTATGTCCCTGTGTATTTATCTGTCTTGAGCGGCAATAGTGGGCTG 1155  
DB 2276 AGTAAAGTTCCTATGTCCCTGTGTATTTATCTGTCTTGAGCGGCAATAGTGGGCTG 2335  
QY 1156 TATGTACTCAAAAGCCGAGGCGCACTTATACACATATGATCTTCAAAAGTTCAGT 1215  
DB 2336 TATGTACTCAAAAGCCGAGGCGCACTTATACACATATGATCTTCAAAAGTTCAGT 2395  
QY 1216 CATCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGTATCATATGCA 1275  
DB 2396 CATCGCAACTGCAAGATGACCAATGTATGTATTAACCCCGGGGTATCATATGCA 2455  
QY 1276 AAATATAGAGAAAGCCGTGTCTTAATAGATTAACCAATCATGCAATGTTTATCTTAA 1335  
DB 2456 AAATATAGAGAAAGCCGTGTCTTAATAGATTAACCAATCATGCAATGTTTATCTTAA 2515  
QY 1336 CGGGATTAATTTAAGGCTCAGTGGGAAATTCAGATGTAATCTTATCAAGAAATATCTCAAT 1395  
DB 2516 CGGGATTAATTTAAGGCTCAGTGGGAAATTCAGATGTAATCTTATCAAGAAATATCTCAAT 2575  
QY 1396 ACAAGATTCAGATTAATTAACAGGCAATCTTATATCTCACTAGCTTGGGAATGT 1455  
DB 2576 ACAAGATTCAGATTAATTAACAGGCAATCTTATATCTCACTAGCTTGGGAATGT 2635

QY 1456 CAACAATCCATCATGATATGCTTTGAATTAAGTATGAGAAAGCAACAGAAATCTAGACA 1515  
DB 2636 CAACAATCCATCATGATATGCTTTGAATTAAGTATGAGAAAGCAACAGAAATCTAGACA 2695  
QY 1516 AGTCAATGTCAAACTGATGACATCATGCTCTCATTAATCTATATGTTTGAATCAT 1575  
DB 2696 AGTCAATGTCAAACTGATGACATCATGCTCTCATTAATCTATATGTTTGAATCAT 2755  
QY 1576 ATCTTTGTTTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635  
DB 2756 ATCTTTGTTTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2815  
QY 1636 GGGGCAACAAAAAATCTTATATGCTTTGGGAAATTAATTAATTAATTAATTAATTAAT 1695  
DB 2816 GGGGCAACAAAAAATCTTATATGCTTTGGGAAATTAATTAATTAATTAATTAATTAAT 2875  
QY 1696 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATTAATTTGTGAAG 1755  
DB 2876 TACAAAATGTGAACACAGATGAGAAAGAAAGTTTCCCTTAATTAATTTGTGAAG 2935  
QY 1756 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 1792  
DB 2936 TTCTGTAGTCTGTCAAGTTCAAGAGTTAAGAAAAA 2972

RESULT 10  
US-11-126-465-1  
: Sequence 1, Application US/11126465  
: Publication No. US20050202045A1  
: GENERAL INFORMATION:  
: APPLICANT: Cochran, Mark D  
: APPLICANT: Cook, Stephanie M  
: APPLICANT: Wild, Martha A  
: TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof  
: FILE REFERENCE: SY01105K10KOK  
: CURRENT APPLICATION NUMBER: US/11/126,465  
: PRIOR FILING DATE: 2005-05-11  
: PRIOR APPLICATION NUMBER: US/09/881,457  
: PRIOR FILING DATE: 2001-06-14  
: PRIOR APPLICATION NUMBER: 09/426,352  
: PRIOR FILING DATE: 1999-10-25  
: PRIOR APPLICATION NUMBER: 08/804,372  
: PRIOR FILING DATE: 1997-02-21  
: PRIOR APPLICATION NUMBER: PCT/US95/10245  
: PRIOR FILING DATE: 1995-08-09  
: PRIOR APPLICATION NUMBER: 08/663,566  
: PRIOR FILING DATE: 1996-06-13  
: PRIOR APPLICATION NUMBER: 08/288,065  
: PRIOR FILING DATE: 1994-08-09  
: PRIOR APPLICATION NUMBER: PCT/US93/05681  
: PRIOR FILING DATE: 1993-06-14  
: PRIOR APPLICATION NUMBER: 08/023,610  
: PRIOR FILING DATE: 1993-02-26  
: PRIOR APPLICATION NUMBER: 07/898,087  
: PRIOR FILING DATE: 1992-06-12  
: NUMBER OF SEQ ID NOS: 5  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 1  
: LENGTH: 3570  
: TYPE: DNA  
: ORGANISM: Newcastle disease virus  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (1194)..(2888)  
: OTHER INFORMATION: NDV Fusion Protein  
: FEATURE:  
: NAME/KEY: misc feature  
: LOCATION: (1355)  
: OTHER INFORMATION: n = any nucleotide  
US-11-126-465-1  
Query Match 50.7%; Score 1701.6; DB 10; Length 3570;  
Best local Similarity 98.4%; Pred. No. 0;

Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;			
Qy	16	TGATCCCGATTGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCTACCAAGAACCC	75
Db	1199	TCGATCCCGATTGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCTACCAAGAACCC	1258
Qy	76	AGCACTATGATGCTGACTATCCGGGTTGCGTGCGCACTGAGTTGCATCTGTCCGGCAAA	135
Db	1259	AGCACTATGATGCTGACTATCCGGGTTGCGTGCGCACTGAGTTGCATCTGTCCGGCAAA	1318
Qy	136	CTCCATTTGATGCGAGGCTCTTTGAGCTGCAAGAAATTTGGTTTCAGAGAACAAAGCCGT	195
Db	1319	CTCCATTTGATGCGAGGCTCTTTGAGCTGCAAG-ACATGTTTACAGAGAACAAAGCAAT	1377
Qy	196	CAACATATACACTCATCCAGACAGATCAATCATAGTTAAGCTCTCCGAAATCTGCC	255
Db	1378	CAACATATACACTCATCTCCAGACAGG-TCAATCAT-TTAAGCTCTCTCCGAAATCTGCC	1435
Qy	256	CAAGGATTAAGGAGCGATGCGAAAGCCCTTGAGTGCATTAACAAGACATTGACCAAC	315
Db	1436	AAAGGATTAAGGAGCGATGCGAAAGCCCTTGAGTGCATTAACAAGACATTGACCAAC	1495
Qy	316	TTTGTCTACCCCTTGTGTACTCTATCCGTAGATTAAGAAGTCTGTGACTACATCTGG	375
Db	1496	TTTGTCTACCCCTTGTGTACTCTATCCGTAGATTAAGAAGTCTGTGACTACATCTGG	1555
Qy	376	AGGGGGGAGACAGGGGCGCTTTATAGCGCCATTATGGCGGTGTGCTCTTGGGGTTGC	435
Db	1556	AGGGGGGAGACAGGGGCGCTTTATAGCGCCATTATGGCGGTGTGCTCTTGGGGTTGC	1615
Qy	436	AACTGCGGCACAAATAACAGCGCGCGCAGCTCTGTATACAGCCAAACAAATGCTGCCAA	495
Db	1616	AACTGCGGCACAAATAACAGCGCGCGCAGCTCTGTATACAGCCAAACAAATGCTGCCAA	1675
Qy	496	CATCTCTCGGACTTTAAGAGACATTTGCCGAACCAATGAGGCTGTGCATGAGTCACTGA	555
Db	1676	CATCTCTCGGACTTTAAGAGACATTTGCCGAACCAATGAGGCTGTGCATGAGTCACTGA	1735
Qy	556	CGGATTTATCGCACTAGCAGTGGCAGTTGGGAAGTGCAGAGTTTGTATATGACCAAT	615
Db	1736	CGGATTTATCGCACTAGCAGTGGCAGTTGGGAAGTGCAGAGTTTGTATATGACCAAT	1795
Qy	616	TAAATAAAACAGCTCAGAAATTAAGCTGCATCAAAATTGCAAGCAAGTTGGTGAAGCT	675
Db	1796	TAAATAAAACAGCTCAGAAATTAAGCTGCATCAAAATTGCAAGCAAGTTGGTGAAGCT	1855
Qy	676	CAACTGTACTTAAACCGAATTGACTACAGTATTCGGACCAACAATCACTTCACTGCTTT	735
Db	1856	CAACTGTACTTAAACCGAATTGACTACAGTATTCGGACCAACAATCACTTCACTGCTTT	1915
Qy	736	AAAAGACTGACTTATTCAGGACCTTTACATCTAGCTGGTGGAAATATGATTAATTAAT	795
Db	1916	AAAAGACTGACTTATTCAGGACCTTTACATCTAGCTGGTGGAAATATGATTAATTAAT	1975
Qy	796	GACTAAGTTAGTGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	855
Db	1976	GACTAAGTTAGTGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC	2035
Qy	856	CGGTAACTTATCTATACAGCTCAAGACTCAACTCTTGGGTATACAGTAACTTAAC	915
Db	2036	CGGTAACTTATCTATACAGCTCAAGACTCAACTCTTGGGTATACAGTAACTTAAC	2095
Qy	916	TTTCAGTGGGAACTTAAATATATGCGTGCACCTACTTGGAAACCTTATCCGTAAGAC	975
Db	2096	TTTCAGTGGGAACTTAAATATATGCGTGCACCTACTTGGAAACCTTATCCGTAAGAC	2155
Qy	976	AACGAGGGATTTTGCCTCGGCACTTGTCCCAAAAAGTGTGACACAGTCCGTTCTGTAT	1035
Db	2156	AACGAGGGATTTTGCCTCGGCACTTGTGTCCCAAAAAGTGTGACACAGGTCGTTCTGTAT	2215
Qy	1036	AGAGAACTTGACACTTCATATCTGTATAGAACTGACTTAAGATTATATTTATACAGAT	1095
Db	2216	AGAGAACTTGACACTTCATATCTGTATAGAACTGACTTAAGATTATATTTATACAGAT	2275

Qy	1096	AGTAACTTCCCTATATGTCCTCGTATTTATTTCTGTGCTTGAAGCGCAATPAGTCGGCTG	1155
Db	2276	AGTAACTTCCCTATATGTCCTCGTATTTATTTCTGTGCTTGAAGCGCAATPAGTCGGCTG	2335
Qy	1156	TATGTACTCAAAAGACCGGACGCTTATACACCAATACATGACTATCAAAAGTTCACT	1215
Db	2336	TATGTACTCAAAAGACCGGACGCTTATACACCAATATATGACTATCAAAAGTTCACT	2395
Qy	1216	CATGCGCACTGCAAGATGACAAATGATGATGTGTAACCCCGGGTATCATATCGCA	1275
Db	2396	CATGCGCACTGCAAGATGACAAATGATGATGTGTAACCCCGGGTATCATATCGCA	2455
Qy	1276	AACTATGAGAACCGGTCTCTATATATGATTAACAATCATGCAATGTTTATCCTTAG	1335
Db	2456	AACTATGAGAACCGGTCTCTATATGATTAACAATCATGCAATGTTTATCCTTAG	2515
Qy	1336	CGGATTAACCTTAAAGCTCACTGGGGAATTTGATGTAACTTATCAAGAAATATCTCAAT	1395
Db	2516	CGGATTAACCTTAAAGCTCACTGGGGAATTTGATGTAACTTATCAAGAAATATCTCAAT	2575
Qy	1396	ACAAGATTCTCAAGTAATTAATPACAGGCAATCTTGATATCTCAACTGAGTTGGGAATGT	1455
Db	2576	ACAAGATTCTCAAGTAATTAATPACAGGCAATCTTGATATCTCAACTGAGTTGGGAATGT	2635
Qy	1456	CAACAACCTGATCAGTAATGCTTTGAATPAGTTAGAGAAACAAACAGAAAATGACAA	1515
Db	2636	CAACAACCTGATCAGTAATGCTTTGAATPAGTTAGAGAAACAAACAGAAAATGACAA	2695
Qy	1516	AGTCAATGTCAACTGACTAGACACATGCTCTCATTAATCTATATCTTTGAGTATCAT	1575
Db	2696	AGTCAATGTCAACTGACTAGACACATGCTCTCATTAATCTATATCTTTGAGTATCAT	2755
Qy	1576	ATCTGTTTGTGTATGTAATGCTTACCTGATTTCTAGCAATGCTACCTAATGTAACAAGAAA	1635
Db	2756	ATCTGTTTGTGTATGTAATGCTTACCTGATTTCTAGCAATGCTACCTAATGTAACAAGAAA	2815
Qy	1636	GGCGCAACAAAACCTTATATGCTTGGGAATATATCTAGATCAGATGAGAGCCAC	1695
Db	2816	GGCGCAACAAAACCTTATATGCTTGGGAATATATCTAGATCAGATGAGAGCCAC	2875
Qy	1696	TACAAAATGTGAACACAGATGAGAACGAAGTTTCCCTTAATATGTAATTTGTGAAAG	1755
Db	2876	TACAAAATGTGAACACAGATGAGAACGAAGTTTCCCTTAATATGTAATTTGTGAAAG	2935
Qy	1756	TTCTGTAGTGTGTCACTTCCAGATTCAGAGTTAAGAAAAA	1792
Db	2936	TTCTGTAGTGTGTCACTTCCAGATTCAGAGTTAAGAAAAA	2972

RESULT 11  
US-10-838-834-19  
; Sequence 19, Application US/10838834  
; Publication No. US20050048074A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, et al.  
; TITLE OF INVENTION: Vectors and Cells for Preparing Immunoprotective Compositions  
; FILE REFERENCE: 3121/2022  
; CURRENT APPLICATION NUMBER: US/10/838, 834  
; PRIOR FILING DATE: 2004-05-04  
; PRIOR FILING DATE: 2003-05-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1734  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
US-10-838-834-19

Query Match 42.7%; Score 1434.4; DB 8; Length 1734;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1438; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1915 ATGACCGCGCCGTTAGCCAAAGTTGCGTTAGAGATGATGAAAGAGAGCAAAAAATACA 1974

Db 1 ATGACCGCGCCGTTAGCCAAAGTTGCGTTAGAGATGATGAAAGAGAGCAAAAAATACA 60

QY 1975 TGGCGCTTGATATTCGCGATTTGCAATCTTATTTCTTAACAGTAGAGACCTTGGCTATATCT 2034

Db 61 TGGCGCTTGATATTCGCGATTTGCAATCTTATTTCTTAACAGTAGAGACCTTGGCTATATCT 120

QY 2035 GTAGCCCTCCCTTTATATAGCATGGGGGCTAGCAACCTAGCGATCTTGTAGGCAATCCG 2094

Db 121 GTAGCCCTCCCTTTATATAGCATGGGGGCTAGCAACCTAGCGATCTTGTAGGCAATCCG 180

QY 2095 ACTAGAGATTCAGGCGAGAAAGAAAGATTAATCATCTACCTGGTCCAAATCAAGATGTA 2154

Db 181 ACTAGAGATTCAGGCGAGAAAGAAAGATTAATCATCTACCTGGTCCAAATCAAGATGTA 240

QY 2155 GTAGATAGGATATATTAAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATTTGTAATCTGAG 2214

Db 241 GTAGATAGGATATATTAAGCAAGTGGCCCTTGAAGTCTCGTTGGCAATTTGTAATCTGAG 300

QY 2215 ACCAATTTATGAAAGCAATTAACATCTCTCTATCATAGATTATAGAGGTCGCAAAAC 2274

Db 301 ACCAATTTATGAAAGCAATTAACATCTCTCTATCATAGATTATAGAGGTCGCAAAAC 360

QY 2275 AGTGGGTGGGGGACCTATTCATGACCAAGATTAATAGGGGAGATAGCAAAAGCTC 2334

Db 361 AGGCGGTGGGGGACCTATTCATGACCAAGATTAATAGGGGAGATAGCAAAAGCTC 420

QY 2335 ATTTAGATATGCTAGTATGTCATCATCTTATCCCTGTGATTTCAAGAACATCTG 2394

Db 421 ATTTAGATATGCTAGTATGTCATCATCTTATCCCTGTGATTTCAAGAACATCTG 480

QY 2395 AATTTATCCGGGCGCTACTACAGATCAGGTTGCACTGGAATACCTCATTTGATG 2454

Db 481 AATTTATCCGGGCGCTACTACAGATCAGGTTGCACTGGAATACCTCATTTGATG 540

QY 2455 AGTGCTACCATTAAGTCTACACCCATATATATATTTGTCTGATGACAGATCACTCA 2514

Db 541 AGTGCTACCATTAAGTCTACACCCATATATATATTTGTCTGATGACAGATCACTCA 600

QY 2515 CATTCATATAGATTTTGAAGCACTTGTGTCTCCGGAATCTGCAACAGGGAGGTATTC 2574

Db 601 CATTCATATAGATTTTGAAGCACTTGTGTCTCCGGAATCTGCAACAGGGAGGTATTC 660

QY 2575 TTTTCACTCTGGTTCATCAACCTGAGCAACCAAAATGGAAAGTCTTGACAGTGTG 2634

Db 661 TTTTCACTCTGGTTCATCAACCTGAGCAACCAAAATGGAAAGTCTTGACAGTGTG 720

QY 2635 AGTGCAACTCCCTGGGTTGTGATATCTGTCTGAAAGTCAAGAGACAGAGAGAA 2694

Db 721 AGTGCAACTCCCTGGGTTGTGATATCTGTCTGAAAGTCAAGAGACAGAGAGAA 780

QY 2695 GATTATTAAGTCACTGTCTCTACGCGGATGATGATGAGAGGTTAGGGTTGACGCGCAG 2754

Db 781 GATTATTAAGTCACTGTCTCTACGCGGATGATGATGAGAGGTTAGGGTTGACGCGCAG 840

QY 2755 TACCAGAAAGAGACCTAGATGTCACAACTTATTCGGGGAATGAGGTCGCAACTACCA 2814

Db 841 TACCAGAAAGAGACCTAGATGTCACAACTTATTCGGGGAATGAGGTCGCAACTACCA 900

QY 2815 GAGATAGGGGGTGGATCTTTTATTTGACAGCGCGATGATGCTTCTAGCTACGAGGCTTA 2874

Db 901 GAGATAGGGGGTGGATCTTTTATTTGACAGCGCGATGATGCTTCTAGCTTACGAGGCTTA 960

QY 2875 AAAACCAATTCACCACTGACACTGTAACAGAAAGAAATATGTATATCAAGCAATAC 2934

Db 961 AAAACCAATTCACCACTGACACTGTAACAGAAAGAAATATGTATATCAAGCAATAC 1020

QY 2935 AATGACACATGCCCAAGTAGCAAGATTAACCAATTTGAAATGGCCAGTCTTGTATAG 2994

Db 1021 AATGACACATGCCCAAGTAGCAAGATTAACCAATTTGAAATGGCCAGTCTTGTATAG 1080

QY 2995 CTTGACGCTTTGGTGGGAAACCATACAGCAGGCTATCTTATTTATCAAGGTCAACA 3054

Db 1081 CTTGACGCTTTGGTGGGAAACCATACAGCAGGCTATCTTATTTATCAAGGTCAACA 1140

QY 3055 TCCTTAGCGCAAGACCCGGTATGACTGTACCGGCCAACAAGTCAACTCATGAGGGGCC 3114

Db 1141 TCCTTAGCGCAAGACCCGGTATGACTGTACCGGCCAACAAGTCAACTCATGAGGGGCC 1200

QY 3115 GAAAGCAGAAATTCACAGTAGAGGACATCTCATTTCTTGTATCAACAGGGGTATCATAC 3174

Db 1201 GAAAGCAGAAATTCACAGTAGAGGACATCTCATTTCTTGTATCAACAGGGGTATCATAC 1260

QY 3175 TTCTCTCCGCTTATTAATCTTATGACAGTCAAGCAAAAGCAACTCTTCAATAGT 3234

Db 1261 TTCTCTCCGCTTATTAATCTTATGACAGTCAAGCAAAAGCAACTCTTCAATAGT 1320

QY 3235 CCTTATCATTCAAATGCTTCACTCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGA 3294

Db 1321 CCTTATCATTCAAATGCTTCACTCGGCGAGGTAGTATCCCTTGCAGGCTTCAGCAAGA 1380

QY 3295 TGCCCAACTCGTGTGTTACTGAGTCTATACAGATCCATATCCCTAATCTTATAGA 3354

Db 1381 TGCCCAACTCGTGTGTTACTGAGTCTATACAGATCCATATCCCTAATCTTATAGA 1440

QY 3355 AACCT 3358

Db 1441 AACCT 1444

RESULT 12

US-10-725-841-1

/ Sequence 1, Application US/10725841

/ Publication No. US20040131640A1

/ GENERAL INFORMATION:

/ APPLICANT: Geerligs, Harmen J.

/ APPLICANT: Brown, Ian H.

/ APPLICANT: Alexander, Dennis J.

/ APPLICANT: Collins, Michael S.

/ TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines

/ FILE REFERENCE: AM100044

/ CURRENT APPLICATION NUMBER: US/10/725, 841

/ NUMBER OF SEQ ID NOS: 2

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 1

/ LENGTH: 1662

/ TYPE: DNA

/ ORGANISM: Paramyxovirus/Newcastle Disease Virus

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)..(1662)

US-10-725-841-1

Query Match 42.1%; Score 1414; DB 7; Length 1662;

Best local Similarity 90.7%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACAGAAACCCAGACACCTATGATGCTATCCGGGTTGCG 106

Db 1 ATGGGCTCCAGACCTTCTACAGAAACCCAGACACCTTGTATGCTGACCGGCTGCGG 60

QY 107 CTGGCACTGAGTTGCACTGTCTCGGCAAACTCCATTTGATGGCAGGCTCTTTCAGAGTGA 166

Db 61 CTGGCACTGAGTTGCGTCTGTCTCGGCAAGTCTCCCTTGATGGCAGGCTCTTTCAGAGTGA 120

QY 167 GGAATTTGTGTTACAGAGACAAAGCGTCAATATACCTTCATCTCCAGACAGATCA 226

Db 121 GGAATTTGTGTTACAGAGACAAAGCAAGTCAATATACCTTCATCTCCAGACAGGTTCA 180

QY 227 ATCATGTTTAAGTCTCTCCCGGAATCTGCCAAGATTAAGAGGCAATGGGAAAGCCGCC 286

Db 181 ATCATGTTTAAGTCTCTCCAAATATGCTCCAAAGATTAAGAGGCGTGTGCAAAAGCCGCC 240



QY 347 AGATACAAAGTCTGTGACTACATCTGAGGGGAGACAGGGGGCGCTTATATAGCGCC 406  
DB 301 AGGTATCAAGAGTCTGTGACTACATCTGAGAGGAGAAAGGGACGCTTATATAGCGCC 360  
QY 407 ATTATGGCGGTGGGCTCTTGGGGTTGCACTGGCCGACAAATTAACAGGGCGCGAGCT 466  
DB 361 ATTATCGCGGTGGGCTCTTGGGGTTGCACTGGCCGACAAATTAACAGGGCTTGGCT 420  
QY 467 CTGATACAAAGCAAAATATGCTGCCAATCCCTCCGACTTAAAGAGAGATGCCGCA 526  
DB 421 CTGATACAAAGCAAAATATGCTGCCAATCCCTCCGACTTAAAGAGAGATGCCGCA 480  
QY 527 ACCATGAGGCTGTGCATGAGGTCACTGACGGAATTTATGCACTACAGAGTGGG 586  
DB 481 ACCATGAGGCTGTGCACGAGGTCACTGATGATATCAAACTACAGAGTGGG 540  
QY 587 AGATGAGAGGTTGTTAATGACCAATTTAATAAAGCTCAAGAAATTGACCTGCATC 646  
DB 541 AGATGAGAGGTTGTTAATGACCAATTTAATAAAGCTCAAGAAATTGACCTGCATC 600  
QY 647 AAAATTCACAGCAAGTGTGTGAGCTCAACCTGTACCTAACGGAATTGACTACAGTA 706  
DB 601 AAAATTCACAGCAAGTGTGTGAGCTCAACCTGTACCTAACGGAATTGACTACAGTA 660  
QY 707 TTGGGACCAACAATCACTTCACTGCTTTAAACAAGCTGACTATTACGCACTTTACAT 766  
DB 661 TTGGGACCAACAATCACTTCCCTCCCTTAAACCAAGCTGACTATCCAGCGCTTTACAT 720  
QY 767 CTGAGTGTGGAATATGATATCTTATGACTAAGTTAGGGAATAACAATC 826  
DB 721 CTGAGTGTGGAATATGATATCTTATGACTAAGTTAGGGAATAACAATC 780  
QY 827 AGCTATTAATCGGTAGCGGCTTATCAACGGTAAACCTTATCTATACGACTCAGACT 886  
DB 781 AGCTATTAATGATAGCGGCTTATCAACGGTAAACCTTATCTATACGACTCAGACT 840  
QY 887 CAACCTTGGGTATACAGTAACTCTAAGTCACTTCACTGCGGAACTTAATATATGCTGCC 946  
DB 841 CAAGCTTGGGTATACAGTAACTCTAAGTCACTTCACTGCGGAACTTAATATATGCTGCC 900  
QY 947 ACCTACTTGGAAACCTTATCCGTAAAGCAACCAAGGGATTTGGCTGGGCACTTGTCCA 1006  
DB 901 ACCTACTTGGAAACCTTGTCTGTAAGTAAACCAAGGATTTGGCTGAGCACTGTGCCA 960  
QY 1007 AAAGTGTGACACAGTCTGCTGTGTATGAGAAAGCTTGACACTTATCTATATGAGAA 1066  
DB 961 AAAGTGTGATGAGAGTCTGCTGTGTATGAGAAAGCTTGACACTTATCTATATGAGAG 1020  
QY 1067 ACTGACTTGAATTTATATTTGTAAGAATAGTAAAGTCCCTATGTCCCTGTATTTAT 1126  
DB 1021 ACCGATTTGATCTATATTTGTAAGAATAGTAAAGTCCCTATGTCTCCGTGTATTTAT 1080  
QY 1127 TCTGTCTTGAAGGGCAATAGTGGGCTGTATGTATCTCAAAAGACCGAAGGGGCACTTACT 1186  
DB 1081 TCTGTCTTGAAGGGCAATAGTGGGCTGTATGTATCTCAAAAGTGAAGGGGCACTTACT 1140  
QY 1187 ACACATATACGACTATCAAAAGTTCAGTCACTGCCAAGTGCAGAGATGACAAACATGTAGA 1246  
DB 1141 ACAGCCGATACGACTCTCAAAAGTTCAGTCACTGCCAAGTGCAGAGATGACAAACATGTAGA 1200  
QY 1247 TGTGTAAACCCCGGGTATCATATGCAAAACTATGAGAGAGCGGTCTCTATATGAT 1306  
DB 1201 TGTGTAAACCCCGGGTATCATATGCAAAACTATGAGAGAGCGGTCTCTATATGAT 1260  
QY 1307 AAACATATACGCAATGTTTATCTTATGCGGGGATTAATTAAAGCTCAGTGGGAAATTC 1366  
DB 1261 AGGCAATATACGCAATGTTTATCTTATGCGGGGATTAATTAAAGCTCAGTGGGAAATTC 1320  
QY 1367 GATGTACTTATCAAGAGATATCTCAATCAAGATCTCAAGTAATATATATGAGGAAT 1426  
DB 1321 GATGTACTTATCAAGAGATATCTCAATCAAGATCTCAAGTAATATATATGAGGAAT 1380  
QY 1427 CTGTATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATAG 1486

DB 1381 CTCGATATCTTCGACTGAGCTTGGGAATGTCAACAACCTCGATTAATATGCTTTGATTAAG 1440  
QY 1487 TTAGAGAAAGCAACAGAAAATAGACAAAGTCAATGTCAAACTGATAGCAATCTGCT 1546  
DB 1441 TTAGAGAAAGCAACAGAAAATAGACAAAGTCAATGTCAAACTGATAGCAATCTGCT 1500  
QY 1547 CTCATTAATCTATATGTTTGTGACTATCATATCTCTTGTGTTTGGTATATAGCTGAT 1606  
DB 1501 CTCATTAATCTATATGTTTGTGACTATCATATCTCTTGTGTTTGGTATATAGCTGAT 1560  
QY 1607 CTAGCATGCTTACCTTAATGTTAACAAGCAAGCGGCAACAAAACCTTATATAGCTGGG 1666  
DB 1561 CTAGCATGCTTACCTTAATGTTAACAAGCAAGCGGCAACAAAACCTTGTATAGCTGGG 1620  
QY 1667 AATATATCTCTAGATCAGATGAGAGCCACTTACAAAATGTGA 1708  
DB 1621 AATATATCTCTGATCAGATGAGAGCCACTTACAAAATGTGA 1662

RESULT 14  
US-09-784-990-10  
; Sequence 10, Application US/09784990  
; Patent No. US20020037292A1  
; GENERAL INFORMATION:  
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE  
; APPLICANT: BOUCHARDON, ANNABELLE  
; APPLICANT: RIVIERE, MICHEL  
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA  
; FILE REFERENCE: 454313-2260  
; CURRENT APPLICATION NUMBER: US/09/784,990  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 96/09339  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: PCT/FR97/01326  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1662  
; TYPE: DNA  
; ORGANISM: Newcastle disease virus  
US-09-784-990-10

Query Match 40.6%; Score 1362.8; DB 3; Length 1662;  
Best Local Similarity 88.7%; Pred. No. 0;  
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTGCG 106  
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTTATGCTGATCATCCGAACGGCG 60  
QY 107 CTGGCACTGAGTGTGATCTGTCTCCGGCAAACTCCATTGATGAGAGGCTTTGGAGCTGCA 166  
DB 61 CTGACACTGAGCTGTATCTGTGACAAAGCTCTTGTATGAGGAGGCTCTTGGCGGTGCA 120  
QY 167 GGAATTTGTTTACAGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGATCA 226  
DB 121 GGAATTTGTTTACAGGAGCAAAAGCCGTCAACATATACCTCATCCAGACAGGATCA 180  
QY 227 ATCATATTAAGTCTCTCCGAACTGTGCCAAGATTAAGAGGCAATGCGAAAGCCCC 286  
DB 181 ATCATATTAAGTCTCTCCGAAATGTGCCAAGATTAAGAGGCAATGCGAAAGCCCCA 240  
QY 287 TTGAGTGCATACAAACAGCAATGACCACTTTGTCTACCCCCCTTGGTACTCTATCTCGT 346  
DB 241 TTGAGGCAATACAAACAGCACTGACTTACTTACTCAACCCCTTGGTATTTCTATCCGC 300  
QY 347 AGATACAAAGTCTGTGACTATCATCTGAGAGGGGGGAGACAGGGGGCGCTTATAGGGCC 406  
DB 301 AGATACAAAGTCTGTGACTATCTTCCGAGAGAGAGAGACAGCGCTTATATAGGTGCC 360  
QY 407 ATTATTTGGCGGTGTGCTCTTGGGGTTGCAACTGCGCACAAATTAACAGCGCGCGAGCT 466



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Db 361 ATATCGGAGGTGAGCTCTTGGGGTTGCGACAGCTGACAGATTAACGACGCTTCGGCC 420
Qy 467 CTGATACAGGCAAAATATGTCGCAACATCTCCGACTTAAAGAGAGAGATTCGGCA 526
Db 421 CTGATACAGGCAAAATATGTCGCAACATCTCCGACTTAAAGAGAGAGATTCGGCA 480
Qy 527 ACCAATGAGGCTGTCATGAGGTCACTGACGATTAATGCAATGACGAGTGGAGTGG 586
Db 481 ACCAATGAGGCTGTCATGAGGTCACTGACGATTAATGCAATGACGAGTGGAGTGG 540
Qy 587 AAGATGCAAGCTTTGTTAATGACCAATTTAAACAGCTCAGGAATTAAGTGCATC 646
Db 541 AAGATGCAAGCTTTGTTAATGACCAATTTAAACAGCTCAGGAATTAAGTGCATC 600
Qy 647 AAATGCAAGCAAGTTGTTGAGGTCAACCGTAACTTAACGATTAAGTGCATCAGTA 706
Db 601 AAATGCAAGCAAGTTGTTGAGGTCAACCGTAACTTAACGATTAAGTGCATCAGTA 660
Qy 707 TTGGAACCAAAATCACTTCACTGCTTAAACAGGTGACTAATTCAGGCACTTAAAT 766
Db 661 TTGGAACCAAAATCACTTCCCTGCTTAACTGAGGTGACTAATTCAGGCTTAAAT 720
Qy 767 CTAGCTGTTGAAATATGATTAATTAATGACTAATGAGTGTAGGGAACATCAATC 826
Db 721 CTAGCTGTTGATATGATTAATTAATGACTAATGAGTGTAGGGAACATCAATC 780
Qy 827 AGCTCAATTAATCGGTAGCGGCTTAATCAACGGTAACTTAATTCAGTCAAGTCA 886
Db 781 AGCTCAATTAATGTTAGCGGCTTAATCAACGGTAACTTAATTCAGTCAAGTCA 840
Qy 887 CAATCTTGGGTTATACAGTAACTCTACCTTCACTGCGGAACTTAATTAATATGCTG 946
Db 841 CAATCTTGGGTTATACAGTAACTCTTCCCTTCACTTGGGAACTTAATTAATATGCTG 900
Qy 947 ACCTACTTGAACCTTATCTGTAAGCAACACAGGGATTTGCTCGGCACTTGTCCA 1006
Db 901 ACCTACTTGAACCTTATCTGTAAGCAACACAGGGATTTGCTCGGCACTTGTCCA 960
Qy 1007 AAATGTTGTAACAGGTGCTGTTCTGTAATGAAAGAACTGACCTCAATCTGTAATGAA 1066
Db 961 AAATGTTGTAACAGGTGCTGTTCTGTAATGAAAGAACTGACCTCAATCTGTAATGAA 1020
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Db 1021 ACCGACTTGAATTAATATGTAACAAGATAGTAAGTTCCTATGTCCTGATTAAT 1080
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Db 1081 TCTGCTTGAAGCGGTAATACGTGCGCTGTATGTAATCAAGACCAAGGCGCACTTACT 1140
Qy 1187 ACACCAATACATGACTATCAAAAGTTCACTGATGCGCACTGCAAGATGACAACTGTAGA 1246
Db 1141 ACCCAATATATGCTTCAAAAGGCTCAGTTATGCTCAATGCAAGCTGCAAACTGTAGA 1200
Qy 1247 TGTGTAACCCCCCGGATATCATATGCAAAACTATGAGAAAGCGTGTCTTAATGAT 1306
Db 1201 TGTGCAATCCCCCGGATATCATATGCAAAACTATGAGAAAGCGTGTCTTAATGAT 1260
Qy 1307 AAACAAATCATGCAATGTTTATCTTATAGCGGGAATTAATTTAGGCTCAAGTGGGAAATTC 1366
Db 1261 AAGGACTCATGCAACGTCTTATCTTATAGCGGGAATTAATTTAGGCTCAAGTGGGAAATTC 1320
Qy 1367 GATGTAATCTATCAAGAAATATCTCAATACAAATTTCTCAAGTAATTAACAGGCAAT 1426
Db 1321 GATGCAACCTATCAAGAAATATCTCAATACAAATTTCTCAAGTAATTAACAGGCAAT 1380
Qy 1427 CTGATATCTCAACTGAGCTTGGGAATGTCAACAACTGATCAGTAATGCTTTGATTAAG 1486
Db 1381 CTGATATCTCAACTGAGCTTGGGAATGTCAACAACTGATCAGTAATGCTTTGATTAAG 1440
Qy 1487 TTAGAGAAAGCAACAGAAATCTAGCAAAAGTCAATGTCAAACTGACTAGCAATCTGCT 1546
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Db 1441 TTAGAGAAAGCAACAGCAAACTAGCAAAAGTCAATGTCAAACTGACCAAGCATCTGCT 1500
Qy 1547 CTCAATTAATTAATGTTTGAATATCAATCTCTGTTTGTGTAATCTTAAGCTGAT 1606
Db 1501 CTCAATTAATTAATGTTTGAATATCAATCTCTGTTTGTGTAATCTTAAGCTGAT 1560
Qy 1607 CTAGATGCTTACCTAATATGTAACAGAAAGGCGCAACAAAACTTATTAATGCTTGGG 1666
Db 1561 CTAGATGCTTACCTAATATGTAACAGAAAGGCGCAACAAAGACTTGTATGCTTGGG 1620
Qy 1667 AATTAATCTAGATCAAGAGAGGCACTTACAAAAATGTA 1708
Db 1621 AATTAATCTTGAATCAAGAGAGGCACTTACAAAAATGTA 1662
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## RESULT 15

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US-10-229-412-10
; Sequence 10, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-229-412-10
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Query Match 40.6%; Score 1362.8; DB 6; Length 1662;  
Best Local Similarity 88.7%; Pred. No. 0;  
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

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Qy 47 ATGGCTCCGACCTTCTACAGAACCCAGACCTTAATGCTGATATCCGGGTTGG 106
Db 1 ATGGCTCCGACCTTCTTACAGGATCCGGTACTCTTAATGCTGATATCCGACCGG 60
Qy 107 CTGGCACTGAGTTGATCTGTCCGCAAACTCAATGAGGCAAGGCTTTGACAGTGA 166
Db 61 CTGACACTGAGCTGTATTCGCTGACAAAGCTCTCTTATATGAGGAGGCTTTGAGGCTGCA 120
Qy 167 GGAATTTGTTTACAGGAGCAAAAGCGGTCAACATATACCTTCATCCAGACAGATCA 226
Db 121 GGAATCTGTTTACAGGAGTAAAGCAGTCAACATATACCTTCATCCAGACAGGCTCA 180
Qy 227 ATCAATTTAAGCTCTCCCGGAATCTGCGCAAGATTAAGAGGATGAGGAAAGCCGCC 286
Db 181 ATCAATTTAAGTATCTCCCGGAATGCGCAAGATTAAGAGGATGAGGAAAGCCGCC 240
Qy 287 TTGATGATATCAACAGAGCAATTTGACCACTTTGCTCAACCCCTTGGTGACTTATCCGT 346
Db 241 TTGAGGCAATCAACAGAGCACTGACCTTATCTTACTCAACCCCTTGGTGAATCTATCCGC 300
Qy 347 AGATACAAAGTCTGTACTCACTTGAAGGGGGAGCAAGGGCGCTTATAGCGCC 406
Db 301 AGATACAAAGTCTGTACTCACTTCCGAGGAAAGAGAGAGACCTTATAGGTTGCC 360
Qy 407 ATTAATGCGGTGCTCTTGGGTTGCAATGCGGCAAAATTAACAGGGCGCGAGCT 466
Db 361 ATTAATGCGGTGCTCTTGGGTTGCAAGCTGCAAGATTAACAGGAGCTTCCGCC 420
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QY	467	CTGATATCAAGCAAAACAAAATGCTGCGCAACATCTCCGACTTAAAGAGAGATTGCCGA	526
Db	421	CTGATACAGCGCAACAGAAATGCTGCGCAACATCTCCGCTTAAAGAGAGATTGCCGA	480
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Db	481	ACCAATGAGGCTGTGCATGAGGTCACTGACGATATTTCACAACTAGCAGTGGCACTTTGGG	540
QY	587	AAGATGCAAGCTTTTGTTAATGACCAATTTTAATTAATAAGCTCAGGAAATTGACCTGATC	646
Db	541	AAGATGCAAGCTTTTGTTCAAATGACCAAGTTCAATTAATAAGGCAAGAAATTGACCTGATTA	600
QY	647	AAATTTGCACGACGAGTGTGTGAGAGCTCAACCTGTACTACCGAATTGACTATACAGTA	706
Db	601	AAATTTGCACGACGAGTGTGTGAGAACTCAACTGTACTATCTGAATTGACTATACAGTA	660
QY	707	TTCCGAGCCACAATCACTTCACTCTGCTTTAAACAAGCTGACTATTTACGAGCACTTACAT	766
Db	661	TTTGGGGCCAAATTCACCTTCCCTGCGCTTAACTGAGCTGACTATTCACGAGCTTTACAT	720
QY	767	CTACCTGTGTGAAATATGATTTACTCTGTGACTAAATTAGGTATGAGGAAACAACAATC	826
Db	721	CTACCTGTGTGAAATATGATTTACTCTGTGACTAAATTAGGTATGAGGAAACAACAATC	780
QY	827	AGCTCATTAATCCGATGAGCGGCTTATCAACGCGTAAACCTTATTTCTATACGACTACAGACT	886
Db	781	AGCTCATTAATTTGATGAGCGGCTTATCAACGCGCAACCTTATTTCTGTACGACTACAGACT	840
QY	887	CAACTCTTGGGTATACAGTAACCTTCACTTCACTGCGGAACTTAATATATATGCGTGC	946
Db	841	CAGATCTTTGGGTATACAGTAACCTTGTGCTTCACTGTTGGAACTGAAATATATGCGTGC	900
QY	947	ACCTACTTTGGAAACCTTATCCGTAAGCAACCAAGGGATTTTGCTCGGCACTTGTCCCA	1006
Db	901	ACCTACTCTGGAGACCTTATCTGTAGCAACAACAAGGATTTTGCTCGCACTTGTCCCA	960
QY	1007	AAAGTGTGACACAGGTGCTTCTGTGATGAAAGAACTTGACACTCTATCTGTATAGAA	1066
Db	961	AAAGTGTGACACAGGTGCTTCCGTATGAAAGAACTTGACACTCTATCTGTATAGAGG	1020
QY	1107	ACTGACTTAGATTTATTTATTTGTACAAAGATAGTAAAGTTCCCTATGTCCCTGATATTTAT	1126
Db	1021	ACGCACTTGGATTTATTACTGTACAAAGATATGATGACATTTCCCTATGTCTCCGTATTTAT	1080
QY	1127	TCTGTCTTGAAGCGGCATATGCTCGGCTGTATGTACTCAAGACCGAAGCGGCACTTACT	1186
Db	1081	TCTGTCTGACGCGTAATACATCGGCTTGCACTGTATTCAAAGACTGAAAGGCGCACTTACT	1140
QY	1187	ACACCATACAGACTATCAAGGTTCAGTATCCGCAACTGCAAGATGACAAACATGTAGA	1246
Db	1141	ACGCACTATATGCGCTCTCAAAAGGCTCAGTATTTGCAATTCGAAGCTGACAAACATGTAGA	1200
QY	1247	TGTGTAAACCCCCGGGATCATATTCGCAAAACTATGAGAGAAGCGGTGCTCTATATAGAT	1306
Db	1201	TGTGTAGATATCCCCCAGATCATATTCGCAAAATTTATGAGAGAAGCTGTGCTCTTATATAGAT	1260
QY	1307	AAACAATCATGCAATGTTTTATTCCTTAGGCGGATATCTTTAAGGCTCAGTGGGAAATTC	1366
Db	1261	AGGCACTCATGCAAGTCTTATTCCTTAGACGGGATTACTCTGAGGCTCAGTGGGAAATTT	1320
QY	1367	GATGTAACTTATTCAGAAAGAAATATCTCAATACAAAGTTCTCAAGTAAATTAATAAGCGCAAT	1426
Db	1321	GATCAACACTATCAAAAGAAATATCTCTATCTAGATTCTCAAGTTATATGTACAGGCAAT	1380
QY	1427	CTGTATATCTCAACTGAGCTTGGGAATGTCAACAACCTGATCAGTAATGCTTTGAAATAG	1486
Db	1381	CTGTATATATCAACTGAGCTTGGGAATGTCAACAACCTAATATAGTAATGCCCTGAATAG	1440
QY	1487	TTAGAGGAAGCAACAGAAAACTAGACAAGAGTCAATGTCAAACTGACTAGACACTTGTCT	1546
Db	1441	TTAGAGGAAGCAACAGCAAACTAGACAAGAGTCAATGTCAAACTGACAGACACTTGTCT	1500
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Accession	Sequence	Length
Db	CTCATTTACACATCGTTTAACTGTCATATCTCTGTGTTTGATGACTTAGCGCTGTT	1560
Qy	CTAGCATGCTACCACTTAATGTAACAAGCAAAAGGCCAACAATAAAACCTTATATGCGCTGGG	1666
Db	CTGACATGCTACCTGATGTAACAAGCAAAAGGCCACAACAAAAAGACTTGTATGGCTTGGG	1620
Qy	AATTAATACTTAGTCAGATGAGAGGCCACTACACAAAATATGTA	1708
Db	AATTAATACCTTGATGATGAGAGGCCACTACAAAATATATGA	1662

Search completed: February 5, 2006, 07:03:34  
Job time : 2559 secs

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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Db 5928 AGATAACACCCGCGATTGCACTTACCAAGTCATGCTGAATCTTCAAGCCATCGACATC 5987
Qy 507 TTAAGAGAGCATTCGCCCAACCAATGAGGCTGTGCATGAGGTCACTGACGATTTATTCG 566
Db 5988 TGAAGAGGAGCTCGAAACTCTATCATGAGCAATTTGAGCAATCAGACCAAGGAGG 6047
Qy 567 AACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTTGTTAATGACCAATTTAATAAACAG 626
Db 6048 AGATGATATTGGCTGTTCAAGGCTGCCAAGCTACATCAATAAAGAGCTGTACCGTCTA 6107
Qy 627 CTCGGAATTAGACTGCATCAAAATTTGACAGAGTTGGTGTAGAGTCAACCTGTACC 686
Db 6108 TGAACCACTATCTTGTGATTTAATCGCCGAAGAGCTGGCTCAAAATGCTCGATAC 6167
Qy 687 TAAACGAATGACTACAGTATTCGAGCAACCAATCACTTCACTGCTTTAAACAAGCTGA 746
Db 6168 ATACAGAAATCTCTCATTTATTTGGCCCAATTTACGGGACCCCATATCTCGGAGATAT 6227
Qy 747 CTATTCAGGCACTTTACATCTAGCTGTGGAAATATGGAATTAATTCTTATGACTAAGTTAG 806
Db 6228 CTATCCAGGCTTTGAGCTATCGCTTGGAGAGACATCAATAGGTGTAGAAAAGCTCG 6287
Qy 807 GTGTAGGGAACAATCACTCACTCATTTAATCGGTAGGCGCTTATCAACCGGTAACTCCTA 866
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Qy 867 TTCTATACGACTCAAGACTCACTCTTGGGTATACAGGTAACTTCACTTCACTGAGTGGGA 926
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Qy 927 AACTAAATATATGCGTGGCCACTTACCTTGAACCTTATCCGTAAAGCAACACGAGGAT 986
Db 6408 AGATTAAGGGGTATGTTCCACCGGCTAGAGGGGGTCTCTTACCAACATAGGCTCTCAAG 6467
Qy 987 TTGCTCGGCACTTGTCCCAAAAGTGTGACACAGGTGCTTGTGATTAAGAAGCTTG 1046
Db 6468 AGTGATATACCACTGTGCTCCAGATATGTGCAACCCAAAGGATCTTATCTGCAATTTTG 6527
Qy 1047 ACACCTCATCTGTATAGAACTGACTTATTAATTTGACAAAGATAGTAACTTCC 1106
Db 6528 ATGAGTATCTGTATCTTTCATGCGAAGGGAGCTGTGTGACGCCAAATTCCTTTATCC 6587
Qy 1107 CTATGTCCTGCTGATTTATTTCTGCTTGAAGGGCAATACGTGGCCTGTATGTACTCA 1166
Db 6588 CGATGATGCTCTCTCCAGAAATGCTCCGGGGGTACACAAATCTCTGCTGTACAC 6647
Qy 1167 AGACCGAAGGCGCTTACATACACATACATGACTATCAAGTTCAAGTCAATGCCCACT 1226
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Qy 1227 GCAAGATGACAAATGTAGATGTGTAAACCCCGGGTATCATATCGCAAAATCTATG 1283
Db 6708 GTGATCAATCTTTGCAAGTGTATACACAGAGATCATATACAAACCTTG 6764

RESULT 2
US-11-155-478A-50
; Sequence 50, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
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; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
US-11-155-478A-50

Query Match 1.3%; Score 43; DB 8; Length 759;
Best Local Similarity 47.3%; Pred. No. 0.0072;
Matches 130; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 411 TTGGCGGTGGCTCTTGGGGTTGCACTCCGCAAAATTAAGCGGCGGCACTCTGA 470
Db 314 TAGGTGAATAGCTCTTGGTGTGCGACAGCAGCAGTCAAGCAGCTTCCGATAG 373
Qy 471 TACAAGCCAAACAAATGCTGCCAATCTCCGACTTAAAGAGCATTGCCCAACA 530
Db 374 CCAAAACATPAGGCTTGAAGTGAATGAATGCAATCAAAAGATGCTCAAAACACA 433
Qy 531 ATGAGCTGTGCATGAGTCACTGACGATTTATCGCACTAGCAGTGGCGGTTGGAGA 590
Db 434 ACAGGCGATATCCACACTAGAAATGAGTGGCAGTCCACCGCAGTAAAGAGC 493
Qy 591 TGCAGCAGTTGTTAATGACCAATTTAATAAACAGCTCAGGATTAGCTGATCAAAA 650
Db 494 TGAAGATTTGTAGCAAAAACCTGACTAGTGAATTAACAAACAAATGTGACATTG 553
Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685
Db 554 CTGATCGAAGATGCTGTGACGTTCACTCATTC 588

RESULT 3
US-11-155-478A-174
; Sequence 174, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 13280
; TYPE: DNA
; ORGANISM: Viruses
; FEATURE:
; OTHER INFORMATION: CAN9875 genomic DNA
US-11-155-478A-174

Query Match 1.3%; Score 43; DB 8; Length 13280;
Best Local Similarity 47.3%; Pred. No. 0.051;
Matches 130; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 411 TTGGCGGTGGCTCTTGGGGTTGCACTCCGCAAAATTAAGCGGCGGCACTCTGA 470
Db 3377 TAGGTGAATAGCTCTTGGTGTGCGACAGCAGCAGTCAAGCAGGATTTGCGATAG 3436
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QY	471	TACAGCCAAACAAATCTGCAACATCTCCGATTAAGAGAGCATTCGCCACCA	530
Db	3437	CCAAACCATTAAGGCTTAGAGTAGAGTGAATGCATCAACAAAGTCTCTCAAAACACCA	3496
QY	531	ATGAGGCTGTGCATGAGGTCACCTGACGGATTATCGCACTAGCAGTGCAGTTGGGAAGA	590
Db	3497	ATGAGGCGAGTATCCACACTAGGAATGGAGTCCGAGTCTTAGCCACCGCAGTAAGAGAGC	3556
QY	591	TGCAGCAGTTTGTATATGACCAATTATTAACAGCTCAGGAATTAGCTGCATCAAA	650
Db	3557	TGAAGAATTTGTGAGCAAAACCTGACTAGTCAATTAAACAAGAAACAATGTGACATTG	3616
QY	651	TTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTAC	685
Db	3617	CTGATCTGAAAGTAGGCTGTCAAGCTTCAGTCAATTTC	3651

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RESULT 4
US-11-155-478A-26
Sequence 26, Application US/11155478A
Publication NO. US20060014140A1
GENERAL INFORMATION:
APPLICANT: Boivin, Guy
APPLICANT: UNIVERSITE LAVAL
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
TITLE OF INVENTION: RESPIRATORY VIRUSES
FILE REFERENCE: 6013-148US
CURRENT APPLICATION NUMBER: US/11/155,478A
CURRENT FILING DATE: 2005-06-20
PRIORITY APPLICATION NUMBER: CA 2,411,264
PRIORITY FILING DATE: 2002-12-19
PRIORITY APPLICATION NUMBER: CA 2,418,004
PRIORITY FILING DATE: 2003-01-24
PRIORITY APPLICATION NUMBER: PCT/CA2003/001994
PRIORITY FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 759
TYPE: DNA
ORGANISM: human, metapneumovirus
FEATURE:
NAME/KEY: gene
LOCATION: (1)...(759)
OTHER INFORMATION: human metapneumovirus, strain Can 98-75
US-11-155-478A-26

```

	Query Match	1.2%	Score 41.4;	DB 8;	Length 759;
	Best Local Similarity	46.9%	Pred. No. 0.023;		
	Matches 129;	Conservative 0;	Mismatches 146;	Indels 0;	Gaps 0;
QY	411 TTGGGGTGTGGCTCTTGGGGTTGCACTCGCCGCAAAATACAGCGCCGAGCTCTGA	470			
DB	314 TAGGTGCAATAGCTCTTGGTGTGGCAAGCAGCAGCATCAGCAGGATTTGGAAATG	373			
QY	471 TACAAGCCAAACAAATATGCTGCCAATCTCCGACTTAAAGAGAGCAATGGCCGACCA	530			
DB	374 CCAAAACCATTAAGCTTGAAGTAGAATGCAATCAAAGGTGCTCTCAAAACACCA	433			
QY	531 ATGAGCTGTGCATAGAGTCACTGACGGATTATGCCAATGACAGTGGCATTTGGGAAGA	590			
DB	434 ACGAGGCGATATCCACACTAGGAATGAGATGCCGATCTTACGCCACCGAGTAAGAGAGC	493			
QY	591 TGCAGCACTTTGTTATATGACCAATTTAATAAAACAGCTCAGGAAATTAGACTGCACAAA	650			
DB	494 TGAAGAATTTGTGTAGCAAAAACCTGACTAGTGAATTTAACAAAGAACAAATGTGCAATTG	553			
QY	651 TTGCACAGCAAGTTGTGTAGAGCTTCAACCTGTAC	685			
DB	554 CTGACCTGAAGATGGCTGTCAAGCTTCAAGTCAATTC	588			

```

RESULT 5
US-11-155-478A-49
; Sequence 49, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; FEATURES:
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No
; OTHER INFORMATION: C-63778
US-11-155-478A-49

```

Query Match	Best Local Similarity	1.2% 46.9%	Score 41.4	DB 8	Length 759
Matches 129	Conservative	0	Mismatches 146	Indels	Gaps 0
Qy	411	TTGGCGGTGTGCTCTTGGGGTTTGCACATGCGGCAAAATATACAGCGGCGGAGCTCTGA	470		
Db	314	TAGGTGCAATAGCTCTTGTTGTGTTTGGCAGAGGAGCGAGTACAGCAGAAATGGAGTATG	373		
Qy	471	TACAAGCCMAACAAATATGCTGCCAACATCTCCGACTTAAAGAGAGCAATGGCCGACCA	530		
Db	374	CCAAACCATTAAGGCTTGAGAGTGAAAGTAATGCATCAAAAGTGTCTCTCAAAACACCA	433		
Qy	531	ATGAGGCTGTGCATGAGGCTCACTGACGGATTATGCGAACTGACGTGCACTTTGGGAA	590		
Db	434	ACGAGGCGAGTATCCACTAGAAATGAGTGCAGTCTTGCCACCCGACTGTAAGAGGC	493		
Qy	591	TGCACAGTTTGTTAATGACCAATTATATAAACAAGCTCAGGAATTAGACTGCATCAAA	650		
Db	494	TGAAAGATTGTGTAGCAAAAACCTGACTAGTGCATTTAACAGAAACAAATGTGCAATTG	553		
Qy	651	TTGCACAGCAAGTTGGTGTAGAGCTCAACTGTATC	685		
Db	554	CTGATCTGAGATGAGCTGTCAAGCTTCAAGTCAATTG	588		

```

RESULT 6
US-11-155-478A-51
; Sequence 51, Application US/11155478A
; Publication NO. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994

```





Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 554 CTGATCTGAAGATGGCTGTGCTGAGCTTCACTCAATTC 588

## RESULT 9

US-11-155-478A-54  
; Sequence 54, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: CA 2,411,264  
PRIOR FILING DATE: 2002-12-19  
PRIOR APPLICATION NUMBER: CA 2,418,004  
PRIOR FILING DATE: 2003-01-24  
PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
PRIOR FILING DATE: 2003-12-19  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54  
LENGTH: 759  
TYPE: DNA  
ORGANISM: human metapneumovirus  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)...(759)  
OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No  
OTHER INFORMATION: C-74501  
US-11-155-478A-54

Query Match 1.2%; Score 41.4; DB 8; Length 759;  
Best Local Similarity 46.9%; Pred. No. 0.023;  
Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 411 TTGGCGGTGTGCTCTTGGGTTGCACTGCCGCAAAATTAACAGCGGCCGAGCTTGA 470  
Db 314 TAGGTGCAATAGCTCTTGGTGTGTCACAGCAGCAGCAGTCAAGGCAATGGGATG 373  
Qy 471 TACAGGCAAAACAATGCTCCCAACATCCCTCCAGCTTAAGAAGAGCAATTGCCGAACA 530  
Db 374 CCAAAACCATTAAGGCTTGAAGTGAAGTGAATGCATCAAAAGGTCTCTCAAAACACCA 433  
Qy 531 ATGAGGCTGTGCTAGAGTCACTGACGATTATGCACTAGCAGTGCAGTTGGGAAGA 590  
Db 434 ACGAGGCAATTCACACTAGAAATGAGTCCAGTCTTAGCCACTGCACTAGAGAGC 493  
Qy 591 TGCAGAGTTTGTATATGACCAATTTAATAAACAAGCTCAGGAATTTAGACTGATCAAAA 650  
Db 494 TGAAGAATTTGTGAGCAAAAACCTGACTAGTCAATTAACAAGAAATGTGACATTG 553  
Qy 651 TTGCACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 554 CTGATCTGAAGATGGCTGTGCTGAGCTTCACTCAATTC 588

## RESULT 10

US-11-155-478A-27  
; Sequence 27, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20

;; PRIOR APPLICATION NUMBER: CA 2,411,264  
;; PRIOR FILING DATE: 2002-12-19  
;; PRIOR APPLICATION NUMBER: CA 2,418,004  
;; PRIOR FILING DATE: 2003-01-24  
;; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
;; PRIOR FILING DATE: 2003-12-19  
;; NUMBER OF SEQ ID NOS: 174  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 27  
;; LENGTH: 759  
;; TYPE: DNA  
;; ORGANISM: human metapneumovirus  
;; FEATURE:  
;; NAME/KEY: gene  
;; LOCATION: (1)...(759)  
;; OTHER INFORMATION: human metapneumovirus, strain Quebec Isolate No  
;; OTHER INFORMATION: C-67345  
US-11-155-478A-27

Query Match 1.2%; Score 41.2; DB 8; Length 759;  
Best Local Similarity 46.8%; Pred. No. 0.027;  
Matches 130; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 408 TTATTGGCGGTGTGCTCTTGGGTTGCACTGCCGCAAAATTAACAGCGGCCGAGCTC 467  
Db 311 TTCTGGGAGCAATAGCACTCGTGTGTCACAGCAGTCAAGGCAATGGGATTTGCAA 370  
Qy 468 TGATCAAGCCAAACAATGCTGCCAATCTCCGACTTAAGAAGAGCAATTGCCGCAA 527  
Db 371 TTGCCAAACCATCGCGCTTGAAGTGAAGTCAACAGCAATTAAGATCCCTCAAAACGA 430  
Qy 528 CCAATGAGGCTGTGCTAGAGTCACTGACGATTATGCACTAGCAGTGCAGTTGGGA 587  
Db 431 CCAATGAAGCAATTCATACATTTGGGAATGAGATTCAGTGTGGCAATCTGCAAGTGAAG 490  
Qy 588 AGATGACAGCTTTGTATATGACCAATTTAATAAACAAGCTCAGGAATTAAGTCAATCA 647  
Db 491 AGCTGAAGAAGCTTTGTGAGCAAGATTTAAGCTGTGCAATCAACAAAACAAGTGCACA 550  
Qy 648 AAATTGACAGCAAGTTGTGTAGAGCTCAACTGTAC 685  
Db 551 TTGATGACTTAATAATGCGCTTGAAGCTTCACTCAATTC 588

## RESULT 11

US-11-155-478A-28  
; Sequence 28, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:

APPLICANT: Bolivian Guy  
APPLICANT: UNIVERSITE LAVAL  
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
FILE REFERENCE: 6013-148US  
CURRENT APPLICATION NUMBER: US/11/155,478A  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: CA 2,411,264  
PRIOR FILING DATE: 2002-12-19  
PRIOR APPLICATION NUMBER: CA 2,418,004  
PRIOR FILING DATE: 2003-01-24  
PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
PRIOR FILING DATE: 2003-12-19  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 759  
TYPE: DNA  
ORGANISM: human metapneumovirus  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)...(759)  
OTHER INFORMATION: human metapneumovirus, strain Can 97-83  
US-11-155-478A-28



```

; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; PRIOR FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 13335
; TYPE: DNA
; ORGANISM: Viruses
; FEATURE:
; OTHER INFORMATION: CAN9783 genomic DNA
US-11-155-478A-173

```

```

Query Match      1.2%; Score 41.2; DB 8; Length 13335;
Best Local Similarity 46.8%; Pred. No. 0.19;
Matches 130; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

```

```

Qy 408 TTATTGGCGGTGGCTTTGGGGTTGCAACTGCCGCAAAATTAACAGCGCCGCACTC 467
Db 3377 TTCTAGGAGCAATGACCTCGTGTTCACACAGCAGCTGACAGTCAACAGAGTGTTCGA 3436

Qy 468 TGAATCAAGCCAAACAAATCTGCAACATCTCCGCTTAAGAGAGCAATTGGCCGA 527
Db 3437 TTGCCAAACCAATCCGGCTTGAAGTGAATGACAGCAATTAAGATCCCTCAAAAACGA 3496

Qy 528 CCAATGAGGCTGTGCATGAGTCACTGACGATTATCGCACTAGCAGTGCAGTTGGGA 587
Db 3497 CCAATGAGGAGTATCTCATTTGGGGAATGAGATTCGAGTGTGCACTGCAATGAGAG 3556

Qy 588 AGATGACAGCACTTTGTTAATGACCAATTTAATAAAACGCTCAGGAATTGACTGATCA 647
Db 3557 AGCTGAAGACTTGTGAGCAAGAAATTAACCTCGTCAATCAACAAAACAAAGTCCGACA 3616

Qy 648 AAATTGCACAGCAAGTGTGTAGAGCTCAACTGTGAC 685
Db 3617 TTGATGACCTTAATAAATGCGCTTAGCTTCACTCAATTTC 3654

```

RESULT 15

```

US-11-155-478A-57
; Sequence 57, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 759
; TYPE: DNA
; ORGANISM: human metapneumovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(759)
; OTHER INFORMATION: human metapneumovirus, strain Quebec isolate No

```

```

; OTHER INFORMATION: hMPV-118
US-11-155-478A-57

```

```

Query Match      1.2%; Score 39.8; DB 8; Length 759;
Best Local Similarity 46.5%; Pred. No. 0.075;
Matches 128; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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Qy 411 TTGGCGGTGGCTCTTTGGGGTTGCAACTGCCGCAAAATTAACAGCGCCGCACTTGA 470
Db 314 TAGTGCAATAGTCTTGTGTGTTCACAGCAGCAGTCAACAGGCAATGGCATAG 373

Qy 471 TACAAGCCAAACAAATGCTGCCAATCTCCGACTTAAGAGAGCAATTGCCCAACA 530
Db 374 CCAAAACCATTAAGGCTTGAAGTGAATGAATGAATCAAAAGTCTCAAAAACACA 433

Qy 531 ATGAGGCTGTGCATGAGGTCACTGACGATTAATGCACTAGCAGTGCAGTTGGGAAGA 590
Db 434 ACGAGGCAATATCCACACTAGAAATGAGATGCGAGTCTTAGCCACCGCAATGAAGAGC 493

Qy 591 TGCAGCACTTTGTTAATGACCAATTTAATAAAACGCTCAGGAATTGACTGCATCAAAA 650
Db 494 TGAAGAATTTGTGAGCAAAAACCTGACCACTGCAATTAACAAGAAATGTGACATTG 553

Qy 651 TTGCAACAGCAAGTTGTGTAGAGCTCAACTGTGAC 685
Db 554 CTGATCTGAAGATGCGTGTCACTTCACTCAATTTC 588

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Search completed: February 5, 2006, 07:13:40  
Job time : 542 secs

Page Blank (uspro)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 21:39:15 ; Search time 12642 Seconds  
(without alignments)  
12427.703 Million cell updates/sec

Title: US-10-800-256-1

Perfect score: 3358

Sequence: 1 acgggtagaagatcttgat.....cctaactctcatagaacc 3358

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues 82156650

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_ges1: \*  
10: gb\_ges2: \*  
11: gb\_ges3: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500.8	14.9	766	7	CK280174 SSH227 SS
2	87.8	2.6	692	2	BG661033 N339 SSH-
3	46.2	1.4	862	2	AZ538746 ENTDM69TF
4	46.2	1.4	886	9	AZ541254 ENTPA11TF
5	43.6	1.3	406	1	AY032979 AY032979
6	43.2	1.3	396	1	AW329422 N200657e
7	43.2	1.3	494	1	AL380807 MCBBS4F09
8	43.2	1.3	670	2	BF641250 NF058C11I
9	42.6	1.3	825	10	C2940314 322053 TO
10	42.6	1.3	1022	11	AL257280 Tetracodon
11	42.4	1.3	507	6	CD081007 MA3-9999U
12	42.4	1.3	816	9	BH183366 023 G.14-
13	42.4	1.3	816	11	AL620907 T7_end of
14	42	1.3	651	7	CK335184 H3150E07-
15	42	1.3	687	5	BY732720 BY732720
16	42	1.3	719	3	BM950384 UI-M-EHPD
17	42	1.3	751	10	CL797382 OR_CBA000
18	41.8	1.2	1085	10	AL101102 Drosophila
19	41.6	1.2	845	10	AL053138 Drosophila
20	41.6	1.2	873	10	C2940484 322268 TO
21	41.4	1.2	551	10	C2784281 OC_Ba014
22	41.4	1.2	680	10	C2835932 OC_Ba021

C	23	41.4	1.2	1101	10	CNS001T2	AL078714 Drosophila
C	24	41.2	1.2	422	5	BU496251	BU496251 PESTOAC0
C	25	41.2	1.2	847	10	CNS0099T	AL053305 Drosophila
C	26	41.2	1.2	878	10	DU094707	DU094707 109747 To
C	27	41	1.2	893	9	BH150882	BH150882 ENTP21TR
C	28	40.8	1.2	1079	5	BX375722	BX375722 BX375722
C	29	40.6	1.2	716	10	CE672698	CE672698 tigr-g85-
C	30	40.4	1.2	670	9	BH158224	BH158224 ENTP70TF
C	31	40.4	1.2	714	9	AQ324694	AQ324694 mgx0019D
C	32	40.4	1.2	801	10	BX213898	BX213898 Danilo rer
C	33	40.4	1.2	894	10	C2950329	C2950329 260379 To
C	34	40.4	1.2	904	10	C2929153	C2929153 246488 To
C	35	40.4	1.2	997	10	C2949863	C2949863 263323 To
C	36	40.2	1.2	779	9	AQ855008	AQ855008 Cpg2035B
C	37	40.2	1.2	825	10	DU057393	DU057393 96348 Tom
C	38	40.2	1.2	865	9	BH180441	BH180441 016 H.20-
C	39	40.2	1.2	865	11	CNS007MAN	AL617393 T3 end of
C	40	40.2	1.2	878	10	CNS0187R	AL108993 Drosophila
C	41	40.2	1.2	1101	10	CNS003FR	AL064653 Drosophila
C	42	40	1.2	529	9	CG853182	CG853182 ND.L.12651
C	43	40	1.2	625	10	C2040511	C2040511 OM_Ba002
C	44	40	1.2	937	10	DU043874	DU043874 158239 To
C	45	40	1.2	1032	10	CNS010NH	AL099191 Drosophila

#### ALIGNMENTS

RESULT 1  
LOCUS CK280174  
DEFINITION SSH227 SSH generated forward (3 days-2 days) subtracted cDNA  
1library Phanerochaete chrysosporium cDNA, mRNA sequence.  
CK280174  
CK280174.1 GI:40556623

ACCESSION BSR.  
Phanerochaete chrysosporium (anamorph: Sporotrichum pulinosum)  
Phanerochaete chrysosporium  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
SOURCES Apophorales; Corticiaceae; Phanerochaete.

ORGANISM 1 (bases 1 to 766)

REFERENCE Uiang,M. and Zhang,Y.  
AUTHORS Screen for Temporal-specific Expression Genes of Phanerochaete  
TITLE chrysosporium Based on SSH and cDNA Microarrays  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yizheng Zhang  
Sichuan Key Laboratory of Molecular Biology and Biotechnology  
College of Life Science, Sichuan University  
Chengdu, Sichuan, box610064 P.R.CHINA  
Tel: 86 028 85412738  
Email: yizhang@scu.edu.cn

SSH generated forward (3 days-2 days) subtracted cDNA library of  
Phanerochaete chrysosporium; average insert size:600 bp;  
Information: Isolation of total RNA from the mycelia incubated in  
shallow stationary culture (Kirk media) at 39\_

Insert Length: 766 Std Error: 0.00

#### FEATURES

POLYA=No.  
Location/Qualifiers  
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/organism="Phanerochaete chrysosporium"  
/molecule="mRNA"  
/strain="BKM-F-1767"  
/db\_xref="taxon:5306"  
/clone\_lib="SSH generated forward (3 days-2 days)"  
subtracted cDNA library  
/note="Vector: pMD18T-vector; SSH generated cDNA library  
of Phanerochaete chrysosporium incubated in N-limited  
shallow stationary culture"

#### ORIGIN

Query Match 14.9%; Score 500.8; DB 7; Length 766;  
Best Local Similarity 84.1%; Pred. No. 9.1e-137;  
Matches 565; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 43 CAGATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGT 102  
| | | | |  
Db 95 CACCATGGGCTCCAACTTTCTACAGAGATCCAGACCTCTGATGCTGATCACCAGAT 154  
| | | | |  
QY 103 TGGCGTGGCACTGAGTTGATCTGTCTCCGGCAAACTCCATTGATGGCAGGCTTTTGACG 162  
| | | | |  
Db 155 TATCTGATATTTGGCGTGTATCCGTCACAGAGCTCTTACCGCAGGCTCTTGACG 214  
| | | | |  
QY 163 TGCAGAAATTTGGTTACAGAGACAAGCGCTCAACATATATACCTCATCCAGACAG 222  
| | | | |  
Db 215 TGCAGAAATTTGATTAACAGAGATTAAGCAGATGATATACCTCTGCTCAGACAG 274  
| | | | |  
QY 223 ATCAATCATAGTTAAGCTCTCCGAAATCTGCCAAGATTAAGAGAGATGCGAAAGC 282  
| | | | |  
Db 275 GTCAATCATAGTCAAGTTGCTCCGAAATATCCGAGGATTAAGAGAGGCTGCGAAAGC 334  
| | | | |  
QY 283 CCCCTTGATGATATACCAAGACATTAACCACTTGTCTACCCCTTGTGATCTCAT 342  
| | | | |  
Db 335 CCCATTAGAGGCAATTAACAGAACCTGACTATTTGCTCACTCTTGTGCGACTCCAT 394  
| | | | |  
QY 343 CCGTAGAGATACAGAGCTGTGACTCATCTGAGAGGGGAGACAGAGGCGCTTATAG 402  
| | | | |  
Db 395 CCGAAGATCCAGAGGCTGTGTCCAGCTCTGAGAGAAAGAGACAAAAACCTTTATAG 454  
| | | | |  
QY 403 CGCATTATTTGGCGGTGTGCTCTTGGGGTTGCAACTGCGCACAAATTAACAGCGCGC 462  
| | | | |  
Db 455 TGTGTTATTTGGCGGTGTAGCTCTTGGGGTTGCAACAGCGCAAGATTAACAGAGCTGC 514  
| | | | |  
QY 463 AGCTCTGATACAGCCAAACAAATGCTGCCAATCTCTCGACTTTAAAGAGACTTGC 522  
| | | | |  
Db 515 GGCCTTATTAACAGCCAAACCGGAATGCGCCAACTCTCGGCTTAAAGAGACTTGC 574  
| | | | |  
QY 523 CGCAACCAATGAGGCTGTGACTGAGGTGACTGACGAGATTAACGAACTAGAGAGTGGAGT 582  
| | | | |  
Db 575 TGCACCAATGAGGTGTGACTGAGGTGACTGACGAGATTAACGAACTAGAGTGGAGT 634  
| | | | |  
QY 583 TGGAGAGTGCAGAGTTTGTAAATGACCAATTTAAATMAACAGTCAAGATTAAGACTG 642  
| | | | |  
Db 635 TGGAGAGTGCAGAGTTTGTCAATGACAGTTTAAATACGCGGCGAAGATTAAGACTG 694  
| | | | |  
QY 643 CATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACTTAACCAATTAAGTAC 702  
| | | | |  
Db 695 TATTAATAATCAACAACAGGTGGTGTAGAACTCAACTATACCTTAATGAATGACTAC 754  
| | | | |  
QY 703 AGTATGCGACC 714  
| | | | |  
Db 755 AGTATCGGGCC 766  
| | | | |

RESULT 2  
BG661033 692 bp mRNA linear EST 26-APR-2001  
LOCUS  
DEFINITION N339 SSH-HCA-U library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG661033  
VERSION BG661033.1 GI:13805211  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 692)  
Zhang, Z. and Dubois, R.N.  
Detection of differentially expressed genes in human colon cancer  
cells treated with NS-398 using suppression subtractive  
hybridization and differential screening  
Unpublished (2000)

JOURNAL  
AUTHORS Contact: Zhonghua Zhang  
TITLE Department of Medicine  
Vanderbilt Medical Center  
COMMENT MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA  
Tel: 615 343 1369

Fax: 615 343 6229  
Email: zhonghua.zhang@mcmail.vanderbilt.edu  
DNA sequencing by: Vanderbilt Medical Center DNA sequencing core  
laboratory. This is a fragment of gene that up-regulated by NS-398  
treatment.  
PCR primers  
FORWARD: 5'-CTAATAGACTCACTATAGGC-3'  
BACKWARD: 5'-TGCAGCGCCGCCCGGACAGT-3'  
Seq primer: M13 forward primer  
High quality sequence stop: 692.  
Location/Qualifiers  
1..692  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="Colon cancer cell"  
/cell\_line="HCA-7"  
/clone\_lib="SSH-HCA-U library"  
/note="Vector: PCR1.1-TOPO, Poly A RNA was isolated from  
NS-398 treated and control cells, and suppression  
subtractive hybridization was performed in forward and  
reverse directions. The adapter sequences used in the  
hybridization were as follows:  
5'-CTAATAGACTCACTATAGGCCTCGACGCGCCGCCGACAGT-3'  
(adapter 1) and  
5'-CTAATAGACTCACTATAGGCGAGCGGTGCGCGCCGAGT-3' (adapter  
2R)."

## ORIGIN

Query Match 2.6%; Score 87.8; DB 2; Length 692;  
Best Local Similarity 48.7%; Pred. No. 7.7e-14;  
Matches 273; Conservative 0; Mismatches 282; Indels 6; Gaps 1;  
QY 219 CAGATCAATCATATATTAAGTCTCTCCGATCTGCCAAGATTAAGAGGATGTGCGA 278  
| | | | |  
Db 132 CAGATCATTTGTGTGTAAGTTAATGCTTCAATTAATGCTGCGGATTAAGTATATA 191  
| | | | |  
QY 279 AAGCCCTTGATGATACATACAGACAGACTTACCTTTGCTACCCCTTGTGACT 338  
| | | | |  
Db 192 TAACATCAATTTCAAGCTATTAATGCAACAGTACAAATCTTACAGCCGATCGTAGA 251  
| | | | |  
QY 339 CTATCCGTAGATACAAAGTCTGTGCTACTACTGTGAGAGGGGAGACAGGGCGCTTA 398  
| | | | |  
Db 252 ATTTGAGACAATTAAGAACAGTTGATTCCACT-----CGAGGAGACGCCGATTTG 305  
| | | | |  
QY 399 TAGCGCCATTAATTTGGCGTGTGCTCTTGGGGTTGCACTGCGCACAATTAACAGCG 458  
| | | | |  
Db 306 CAGGGGTGTGATTTGATTTAGTGTGATTAAGATAGTACTTCCGCAAGGTCTCGG 365  
| | | | |  
QY 459 CCGAGCTGTGATACAGCCAAACAAATGCTGCAACATCTTCCGACTTAAAGAGCA 518  
| | | | |  
Db 366 CAGTACACTAGTAAAGCAAAATGAATGCTCGGCTATATCTCAATCTCAAAATGCAA 425  
| | | | |  
QY 519 TTGCGGCAACCATGAGGCTGTGATGAGTCACTGACGATTAATGCCAATCTGCACTGG 578  
| | | | |  
Db 426 TCCAAAAACAAATGCGGAGTTGCAACGCTGTGTCAGGCGCACCAATCTAGAAACGG 485  
| | | | |  
QY 579 CAGTTGGAGATGACAGAGTTTGTATATGACCAATTAATTAACAGCTCAGGAATTAG 638  
| | | | |  
Db 486 CAGTTCAAGAGTTCAAGATCATTAACAGTGTGTAGTCCAGCAATTAACAGACCA 545  
| | | | |  
QY 639 ACTGCATCAAAATTTGCACAGCAAGTTGTTAGTCAACCTGTACCTTAACCGAATTGA 698  
| | | | |  
Db 546 ACTGTAGGCCCAAGAGTGTATATGCTCAATCTCAATCTTATTTAGCGAGTTGA 605  
| | | | |  
QY 699 CTACAGTATTTGGAACCAATCATCTTACCTGTTTAAACAGGTACTATTCAGGCAC 758  
| | | | |  
Db 606 CAACTATCTTCCCAATCAATTAACAAACCTGATTAAGTCTTATTAACATTCAGCTT 665  
| | | | |  
QY 759 TTTACATCTAGCTGTGGA 779  
| | | | |  
Db 666 TAAGGATTTACTGGGAGTA 686  
| | | | |





AY032979/c  
LOCUS AY032979 406 bp mRNA linear EST 03-MAY-2002  
DEFINITION AY032979 upregulated by angiotensin II in mesangial cells Homo  
sapiens cDNA clone Angm-52f, mRNA sequence.  
ACCESSION AY032979  
VERSION AY032979.1 GI:20429781  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 406)  
Zhou, A., Zhang, H. and Wang, H.  
Cloning and identification of a novel gene up-regulated in human  
mesangial cells stimulated by angiotensin II  
Unpublished (2002)  
Contact: Zhou, A., Zhang, H. and Wang, H.  
Institute of Nephrology  
Peking University  
No. 8, Xishiku St., Beijing, 100034, P. R. China.  
Location/Qualifiers  
1..406  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="Angm-52f"  
/clone\_1b="upregulated by angiotensin II in mesangial  
cells"  
FEATURES  
source  
ORIGIN  
Query Match 1.3%; Score 43.6; DB 1; Length 406;  
Best Local Similarity 47.2%; Pred. No. 0.91;  
Matches 133; Conservative 0; Mismatches 149; Indels 0; Gaps 0;  
QY 401 GGCGCATTAATGGCGGTGCTCTTGGGGTTCGAATGCGGCAATTAACGCGGC 460  
DB 282 GGGGCGGTCATCGGTGAGTTGTCATTAAGGGGTGCGGTCAGGCGGATTAACGCGG 223  
QY 461 GCAGCTGTATCAAGGCAAAATGCTGCCAATCTCGGACCTTAAGAGAGATT 520  
DB 222 GTTGCTTCAACATCTCATTCAATGCAATGCTATTTTGACATCAAGATTCTATC 163  
QY 521 GCCGCAACATGAGCTGTGTCATGAGTCACTGACGATTAATGCAATGAGTGGCA 580  
DB 162 AGCAGCTTAACAAGCAATTAACAAGATTCAACACATGCTGCTGCTG 103  
QY 581 GTTGGGAATGACGAGTTGTTAATGACCAATTAATAAAGCTCAGGAATTAGAC 640  
DB 102 TTAATGCTCTCCAGGACAGATTAATCAATGAGTGGCCGAGCTATTAATTTCTAGGA 43  
QY 641 TGCATCAAAATTGACAGCAAGTTGCTGAGTCAAGCTGACCTG 682  
DB 42 TGCAGGTGCTGTAATGACTAGTCTAAATTAATTAACAG 1  
RESULT 6  
AM329422 386 bp mRNA linear EST 01-MAY-2000  
LOCUS AM329422  
DEFINITION N200857e rootphos(-) Medicago truncatula cDNA clone MHRP-19H9, mRNA  
sequence.  
ACCESSION AM329422  
VERSION AM329422.1 GI:6800017  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 386)  
Harrison, M.J., Liu, J., Harris, A.R., Scott, A.D., Gonzalez, R.A.,  
Gonzalez, M.B. and Ellis, L.

TITLE ESTs from phosphate starved roots  
JOURNAL Unpublished (1999)  
COMMENT Contact: Harrison M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7380  
Email: mjharrison@noble.org  
Date: 1/23/00; Updated to the Database of Expressed Sequence Tags  
(dbEST) on 04/27/00; More information is available at  
'http://chryslie.tamu.edu/medicago'.  
Seq primer: T3.  
FEATURES  
source  
Location/Qualifiers  
1..386  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cullivar="Jemalong, line A17"  
/db\_xref="taxon:3880"  
/clone="MHRP-19H9"  
/issue\_type="rootlet"  
/dev\_stage="phosphate starved"  
/clone\_1b="rootphos(-)"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; At the trifoliolate stage, M. truncatula plants were  
transplanted to phosphate-free sand and grown for a  
further 30 days. During this 30 day period, they were  
fertilized twice weekly with 1/2 Hoaglands solution  
containing only 20uM potassium phosphate. RNA was prepared  
from the roots. cDNA was prepared from polyA+ enriched  
RNA. The cDNA was directionally ligated into the Unizap XR  
vector from Stratagene and packaged using Gigapack III  
Gold packaging extracts. Plasmids containing cDNA inserts  
were excised from the recombinant lambda-zap phage using  
Ex-assist helper phage and propagated in SOLR cells."  
ORIGIN  
Query Match 1.3%; Score 43.2; DB 1; Length 386;  
Best Local Similarity 50.0%; Pred. No. 1.2;  
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;  
QY 1394 ATCAAGATTCTCAAGTAATTAATTAACAGGCAATCTGATCTCACTGAGCTTGGGAAT 1453  
DB 81 ATAGCATTAACCTTACCAATTAATGCTAAATGAATTAATTCACAGTGTGTTAGT 140  
QY 1454 GTCAACACTCGATCGATTAATGCTTGAATTAATGAGGAAGCAAGAAACTAGAC 1513  
DB 141 GTTAACATGCTGATCAAGAACATGAATGTTGTTCCGAAGAGACAGAAAGAGAG 200  
QY 1514 AAGTCATGTCAACTGACTAGACATGCTCTCATTAACCTATATCGTTTGACTATC 1573  
DB 201 AGATCAAGTTTGAATATCTTCTTAACGGAAGCTTTGTAAAGTTGTGATGAATC 260  
QY 1574 ATATCTCTTGTGTTGTTGATTAATCTTACCTGATTTCTA 1609  
DB 261 ATACGTTTGAATTAATGTTGCTTTTGTGACCTTTA 296  
RESULT 7  
AL380807 494 bp mRNA linear EST 03-AUG-2000  
LOCUS AL380807  
DEFINITION MCBBS4F09R1 MBBB Medicago truncatula cDNA clone MCBBS4F09 T7, mRNA  
sequence.  
ACCESSION AL380807  
VERSION AL380807.1 GI:9680559  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 494)

**AUTHORS** Journet, E.P., Crespeau, H., van Tuinen, D., Gouzy, J., Jallou, O., Mebel, A., Carreau, V., Chataigner, O., Kahn, D., Glanville, Pearson, V., and Gamas, P.

**TITLE** Medicago truncatula ESTs from Sinorhizobium meliloti-induced root nodules

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 33326 Castanet-Tolosan Cedex, France (Email: Mc-est@toulouse.inra.fr Website: http://sequence.toulouse.inra.fr/Mtruncatula.html).  
Location/Qualifiers

**FEATURES** source  
1..494  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="Jemalong"  
/db\_xref="taxon:3880"  
/clone="MCB54P09"  
/tissue\_type="symbiotic root nodules"  
/dev\_stage="harvested 4 days post inoculation with Sinorhizobium meliloti"  
/note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2: XhoI; Plants were grown in an aeroponic chamber on nitrogen-rich medium for 21 days. Three days before inoculation with Sinorhizobium meliloti, the medium was replaced by N-free medium. Root nodules (+ short adjacent root segments) were harvested 4 days post inoculation. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from stragene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exsacit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

**ORIGIN**

Query Match 1.3%; Score 43.2; DB 1; Length 494;  
Best Local Similarity 50.0%; Pred. No. 1.3;  
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1394 ATACAAGATTCTCAAGTAATATAACAGCAATCTTGATATCTCAACTGAGCTGGGAT 1453  
DB 190 ATAGCATTAACCTTAGCAATATGCTGTAATGATATCTCACACGCGCTTAGGT 249  
QY 1454 GTCAACAACCTGATCAGTAATGCTTGATAGGAAAGCAAGAAACTAGAC 1513  
DB 250 GTAACAATCGTGTCAGAACACAAATGATGTTCTGGAAGAGACAGAAAGAG 309  
QY 1514 AAAGTCATGCAACTGATAGCAATCTGCTCATTAACCTATATCGTTTGAATATC 1573  
DB 310 AGATCAAGTTGTAAATATCTTTTAACGGAAGCTTTGTAAGTTGTGTAAATC 369  
QY 1574 ATATCTCTGTTTGGTATACCTTAGCTGATCTTA 1609  
DB 370 ATACGTTTGAAGTTAGTTCTTTTGGACTTA 405

**RESULT 8**  
BF641250/c 670 bp mRNA linear EST 19-DEC-2000  
LOCUS NF058C11IN1F085 Insect herbivory Medicago truncatula cDNA clone  
DEFINITION NF058C11IN 5', mRNA sequence.  
ACCESSION BF641250  
VERSION BF641250.1 GI:11905408  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

**AUTHORS** Korth, K., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.

**TITLE** Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: kthor@comp.uark.edu  
Insert Length: 670 Std Error: 0.00  
Plate: 058 row: C column: 11  
Seq primer: TCACACAGAAACAGCTATGAC.

**FEATURES** source  
1..670  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF058C11IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

**ORIGIN**

Query Match 1.3%; Score 43.2; DB 2; Length 670;  
Best Local Similarity 50.0%; Pred. No. 1.4;  
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1394 ATACAAGATTCTCAAGTAATATAACAGCAATCTTGATATCTCAACTGAGCTGGGAT 1453  
DB 241 ATAGCATTAACCTTAGCAATATGCTGTAATGATATCTCACACGCGCTTAGGT 182  
QY 1454 GTCAACAACCTGATCAGTAATGCTTGATAGGAAAGCAAGAAACTAGAC 1513  
DB 181 GTAACAATCGTGTCAGAACACAAATGATGTTCTGGAAGAGACAGAAAGAG 122  
QY 1514 AAAGTCATGCAACTGATAGCAATCTGCTCATTAACCTATATCGTTTGAATATC 1573  
DB 121 AGATCAAGTTGTAAATATCTTTTAACGGAAGCTTTGTAAGTTGTGTAAATC 62  
QY 1574 ATATCTCTGTTTGGTATACCTTAGCTGATCTTA 1609  
DB 61 ATACGTTTGAAGTTAGTTCTTTTGGACTTA 26

**RESULT 9**  
C2940314/c 825 bp DNA linear GSS 11-AUG-2005  
LOCUS C2940314 322053 Tomato Ecori BAC library Lycopersicon esculentum genomic clone SL Ecori0012A21 5, genomic survey sequence.  
DEFINITION C2940314  
ACCESSION C2940314  
VERSION C2940314.1 GI:72273291  
KEYWORDS GSS.  
SOURCE Lycopersicon esculentum (Solanum lycopersicum)  
ORGANISM Lycopersicon esculentum  
DEFINITION Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 825)  
REFERENCE Mueller, L.A., Buel, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J., Van Eck, J. and Stack, S.

TITLE	BAC end sequencing from three Solanum lycopersicon libraries
JOURNAL	Unpublished (2005)
COMMENT	Other_GSSs: 308295

**ORIGIN**

Query Match	1.3%	Score	42.6	DB	10	Length	825
Best Local	Similarity	51.9%	Pred. No.	2.4			
Matches	96	Conservative	0	Mismatches	89	Indels	0
						Gaps	0

QY	1357	TGGGAAATTCGATGAACTTATACGAGAAATATCTCAATACAAAGTTCTCAAGTAATAT	1418
Db	526	TGCTTAATTCGGTATTACTTAGCCATTAGCCAAATTTATATATATTTTAAAAAACATT	467
QY	1417	AACAGGCATCTTGATATCTCACTGACCTTGGGATGTCACCAACTGATCAGTAATGC	1478
Db	466	GTGAGCCAAATTTTGGCATAGACTAATCTTGACATATTTATGGAAATCTGAAATATGTG	407
QY	1477	TTTGAAATBAGTTAGAGGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAG	1538
Db	406	TAAACAATTTATTTGGCAGAAAGCAAACTTTCACTAGACAAATGGTCATGAGAAATATCATTAG	347
QY	1537	CACAT	1541
Db	346	CTAAT	342

RESULT 10	CNS03RIF/c	LOCUS	DEFINITION
CNS03RIF	1022 bp	DNA	linear
Tetradon nigroviridis genome survey sequence, PUC-ORI end of clone 049L07 of library G from Tetradon nigroviridis, genomic survey			

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS
1	Roest Croollius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Pizanes, C., Wincker, P., Brotier, P., Quetier, F., Saurin, W. and Weissenbach, J.	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence	Nat. Genet. 25 (2), 235-238 (2000)	10835645	2	Roest Croollius, H., Jalllon, O., Dasilva, C., Ozouf-Costaz, C.,

**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)

## ORIGIN

Query Match	1.3%;	Score 42.6;	DB 11;	Length 1022;
Best Local Similarity	49.3%;	Pred. No. 2.6;		
Matches 111; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0;

Qy	1360	GGAAATTCGAATGAACTTATCAGAAAGATATCTCAATCAAGATTTCTCAAGTAAATTAATAC	1419
Db	837	GGATTAGAAATTACCGACCAAAATTATTTCTATGCTAAATGGCAAGTAATGAAAG	778
Qy	1420	AGGCATCTTGATATCTCAACTGAGCTTGGGAATGTCACAACCTCGATCAATGCTTT	1479
Db	777	GAGAAATCTGATTAATCTTCCCAAGAGTCGAAAGTTTGCACTATTAATTAAGCCCTTT	718
Qy	1480	GAATTAAGTTGAGAAAGCAACGAAACATAGACAAGTCATGTCAAACCTGACTAGAC	1539
Db	717	AAACAAATTTGGGGAAGCCCAAGTGATTAATGTCACTACCTTGGAAATTAATTAAGAAAGTCTC	658
Qy	1540	ATCTGCTCATTAACCTATATCGTTTGAATATCATATCTCTTGT	1584
Db	657	TGATAGGTTTAATTAAACAACATGGTTCATCTTTTCAACAATTAAT	613

RESULTS	DEFINITION	LOCUS	CD081007	CD081007	RESULT 11
MA3-9999U-M317-D07.G, mRNA sequence.	MA3-9999U-M317-D07.U.G MA3-0001 Schistosoma mansoni CDNA clone	507 bp	linear	EST 14-SEP-2003	

REFERENCE	AUTHORS
1 (bases 1 to 507)	
	Verjovski-Almeida, S., Demarco, R., Martins, E. A. L., Gutmaraes, P. E. M., Ojopi, E. P. B., Paquola, A. C. M., Piazza, U. P., Nishiyama, M. Y. Jr., Kitajima, J. P., Adamson, R. E., Ashton, P. D., Bonaldi, M. F., Coulson, P. S., Dillon, G. P., Fairis, L. P., Gregorio, S. P., Ho, P. L., Leite, R. A., Malaguas, L. C. C., Marques, R. C. P., Miyasato, P. A., Nascimento, A. L. T. O., Ohlweiler, F. P., Reis, E. M., Ribeiro, M. A., Sa, R. G., Stukart, G. C., Soares, M. B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A. M. B. N., Wilson, R. A., Menck, C. F. M., Setubal, J. C., Leite, L. C. C. and Dias-Neto, E.
TITLE	Transcriptome analysis of the acclimated human parasite <i>Schistosoma</i> <i>mansoni</i>
JOURNAL	Nat. Genet. 35 (2), 146-157 (2003)



FEATURES

source

location/Qualifiers

1. .816

/organism="Schistosoma mansoni"

/mol\_type="genomic DNA"

/strain="Puerto-Rican"

/db\_xref="taxon:6183"

/clone="023BD07"

/clone\_lib="SmbAC1"

/note="End : 17"

ORIGIN

Query Match 1.3%; Score 42.4; DB 11; Length 816;

Best Local Similarity 35.8%; Pred. No. 2.7;

Matches 81; Conservative 41; Mismatches 104; Indels 0; Gaps 0;

QY 1375 TTATCAGAGAATTCATCATACAGATTCCTCAAGTAATTAATACAGCAATCTTGATAT 1434

Db 536 TTACAGAAAAAANNATATATATATATTAATTAATAAATATTAATAAATATATATATAT 477

QY 1435 CTCACAGAGCTTGGGAATGTCACAACATCATCATAGTAATGCTTGAATAGTAGAGA 1494

Db 476 ATATATATTAANAATAAATAATATTAATTTTATATTAATAAAGAAAAAATAAAAAAAN 417

QY 1495 AAGCAACGAAAACTAGACAAGTCAATGTCAAACTGACATGCTCATCTCATATAC 1554

Db 416 AAAAAAAATTAAGTAAATTAATAAAAAAATAAAAAAATAAATTAATTAATTAATTAATTA 357

QY 1555 CTATATGCTTTTGTGACTATCATATCTCTGTTTTTGGTAATCTTAAAC 1600

Db 356 YGYBYBYKYTKYTGTTGTGKTGKTGTGBCBCKMGGYAGC 311

RESULT 14

CK35184/

LOCUS

DEFINITION

CK35184 651 bp mRNA linear EST 22-DEC-2003

ACCESSION

CK35184

VERSION

CK35184.1 GI:40290797

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Tanaka,T.S., Jardacat,S.A., Jim,M.K., Kargul,G.J., Wang,X., Grabovac,M.J., Pantano,S., Sano,Y., Iiao,Y., Nagasaja,R., Dol,H., Wood,W.H., Ilt, Becker,K.G. and Ko,M.S.H.

TITLE

Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

COMMENT

10922068

Contract: Dawood B. Dudekula

Laboratory of Genetics

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Email: cdna@igsun.gfc.nia.nih.gov

Plate: H3150 row: E column: 07

Seq primer: M13 Reverse

High quality sequence stop: 651

POLYA=No.

location/Qualifiers

1. .651

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 /notes="Vector: pSPORT1, Site 1: SalI, Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

Query Match	1.3%	Score 42	DB 7	Length 651
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**TITLE**  
**JOURNAL**  
**PUBMED**  
**COMMENT**

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carinici, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akiyama, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 12466851  
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 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, T., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

**FEATURES**  
**source**

location/Qualifiers  
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**ORIGIN**

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 Job time : 12647 secs



**FOR THE**